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| E28872 Xylanase ge | Continuation (15 o | AY795559 Thermobif | S67387 xln2=endoxy | AR055687 Sequence | X69573 T.reesei xy | AL115832 Botrytis | D49850 Chaetomium | AY575961 Gibberell | AR441840 Sequence | AR369734 Sequence | AR274543 Sequence | AJ508952 Nonomurae | AJ863566 Gibberell | AF194025 Streptomy | L13596 Cochliobous | M64552 Streptomyce | A62443 Sequence 5 | X98518 Streptomyce | 268891 A.pisi endo | AB110644 Streptomy | AL939112 Streptomy | CQ786060 Sequence | D49851 Chaetomium | AJ292317 Streptomy | AY551187 Aspergill | AF490982 Aspergill |

ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL FEATURES RESULT 1 AR044575 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM B Ś S 망 5 뫄 S 밁 \$ ORIGIN Query Match Best Local Similarity Matches 983; Conserv source Wunknown. M Unclassified. E 1 (bases 1 to 983) E Hansen, P.Kamp., Wagner, P., Mulical Animal feed additives Animal feed additives Location/Qualifiers 1. .983 'organism="unknown" 241 181 121 61 61 AR044575 Sequence 1 : AR044575 AR044575.1 TCGGCCCGACGTCTTGCAATCCTTGCAGTGATGGTCGGCTTTACCCCC TCGGCCCGACGTCTTGCAATCCTTGCAGTGATGGTCGGCTTTACCCCC GACGGTGGAGCGCAGGCCACGTACACCCAACCTGGAAGGCGGCACCTAC CGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTA CGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTA1 GCCTTAGCCGCGACTGGGGCCCTGGCCTTCCCCGGCAGGGAATGCCACC GGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTTGGAACCCCCGGCCTGAACGCAAGAGCC 300 GACGGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGG 240 100.0%; Score 983; DB 6; larity 100.0%; Pred. No. 7.8e-223; Conservative 0; Mismatches 0; from patent GI:5966040 SD 983 bp S 5817500. Þ and Length Knap, Indels linear н 983; .Helmer. GAGATCAGCTGG 240 GAGCTCGAAAAG 120 GTTGCCCTTGCG 60 GAGCTCGAAAAG 120 CCTGGTGGAGT 180 CCTGGTGGAGT 180 PAT 29-SEP-1999

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| tch 100.0%; Score 983; DB 6; Length 983; | ia ch | Hansen, P.Kamp., Wagner, P., Mullertz, A. and Knap, I.Helmer. Animal feed additives Patent: US 6245546-A 1 12-JUN-2001; Location/Qualifiers | ied. | Sequence 1 from patent US 6245546. AR157660 AR157660.1 GI:16218623 | OR3 to DAT 17 | 961 AAAAAAAAAAAAAAAAAAAA 983 | 901 TTGTTATTGCTTCGTTGTCTAGTGTACATAGCCGAGCAATTGAGGCCTCACGCTTGGGAA 960 | 841 GAGCCTGGCCAGGATCAGTAGTTGCTTTTGCGGTGTTTTGCTCCTATTCTCGTGAAAAAA 900 | 781 ATCAGCATATCTGTCTGCCCTTGCGAGTGATACTTTGGAGGACTGTGGAGAACTTTGTGC 840 | 721 TGGTGATCTCGCGAGGCAACAGCCAAGAATGTCGTCAGATGTGCCGGTTGAAGGTATTCA 780 | 661 TACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGCTAAGACGTAACCTGG 720 | 601 GCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGC 660 | 541 GTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCCACTTCGACGCCTGG 600 | 481 ACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCTTCGACCAATACTGGTCG 540 | 421 TCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAG 480 | 61 ACCCGCAACCCGCTGGTCGAGTATTACATCGTCGAGAACTTTGGCACCTATGATCCTTCC 420 | 01 ATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGG 360 | |
| RESULT 3 | Qy Db | Qy db | dy Qy | dd VQ | dg dg | 4d 45 | dg VQ | Qy Db | Qy Db | Qy Db | Qy Db | Qy Db | dy Qy | Qy Db | Qy Db | dd Ab | dd YQ | 3 H |
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Schlacher, A., Holzmann, K., Hayn, M., Steiner, W. and Schwab, H. Schlacher, and Chwab, H. Cloning and characterization of the gene for the thermostable xylanase XynA from Thermomyces lanuginosus
J. Biotechnol. 49 (1-3), 211-218 (1996)
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Schlacher,A., Holzmann,K., Hayn,M., Steiner,W. and a
Schlacher,A., Holzmann,K., Hayn,M., Steiner,W. and a
Direct Submission
Submitted (06-SEP-1995) Institute of Biotechnology,
Biocatalysis, TU-Graz, Petersgasse 12,, Graz 8010,
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llarity 89.8%;
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Xylanase variants having altered sensitivity

Patent: WO 0166711-A 9 13-SEP-2001;

DANISCO A/S (DK)
                                                                                      Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
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                        Aign, V., Hoheisel, J., Nyakatura, G., Mewes, H.
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                           Fartmann,B.,
haupt,G.
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AUTHORS
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RS German Neurospora genome, project.
Direct Submission
AL Submitted (26-NOV-2003) MIPS, Institut fuer Bioinformatik,
GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH,
Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail:
G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute
of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf,
E-mail: ulrich-schulte@uni-duesseldorf.de
BAC clone 10D6 (strain OR74A) is available at the Fungal Genetic
Stock Center, http://www.fgsc.net
Sequencing was performed by MWG Biotech AG, Ebersberg, Germany,
http://www.mwgdna.com
Information on performance of analysis and a more detailed
annotation of this entry and other sequences can be viewed at:
http://mips.gsf.de/proj/neurospora.
Location/Qualifiers
1. .89019
'~~~~~~**nem="Neurospora crassa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
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VIDRPDNGIAYVQPHGGL
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CCCTTCGTCGGGCGCCCAACGTCTCGGATCCGTCTACACCGACGGCTCCACCTACGACAT
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Length
            89019;
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AAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCT CTGGACCGACAACGGCGCAATGTCAACTACGCCAACGGCGCCCAGCGGCTCTTACTCTGT 39163 CCTCCTCGGCGCTGCCGGTGCCCTCGCTATGCCCCTTCAACGCCACCGAGTTCTCTGAGCT 39283 TCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACT CAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCC GAACTGGCAGAACGCCGGCAACTTTGTCGCCGGCAAGGGCTGGAACC GTGGAGTGACGGTGGAGCGCACGTACACCAACCTGGAAGGCGGCACCTACGAGAT CGCCGAGCGTGGCGGTACCCCCCAGCAGCACCGGCTTCAACAACGGCT CGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTT CGGTTGGACCCGCAACCCGCTGGTCGAGTATTACATCGTCGAGAACT TCGCACCATCACCTACTCGGGTAACTTCAGACCCTCGGGCAACGGCT CCTTGCGGCCTTAGCCGCGACTGGGGCCCTGGCCTTCCCGGCAGGGAATGCCACGGAGCT 113 26.7**%**; Score 262.4; DB 15; Pred. No. 2.1e-51; 0; Mismatches 216; Indels ACCTGTCCGTCTA TCTACTACTCCTT ATTACTATTCCTG ACCITGCGGTCTA 353 TGGCTCCTACAA TGGCACCTATGA 413 CGGTTCG---GC CGGCCTGAACGC 6 Gaps 39106 473 39046 293 233 39223 38986 173 2

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DEFINITION
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Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sor.
Hypocreomycetidae; Hypocreales; Hypocreaceae; D.C., Pretorius, I.S. and van Zyl, W.H.
Expression of a Trichoderma reesei beta-xylanase; Saccharomyces cerevisiae
Appl. Environ. Microbiol. 62 (3), 1036-1044 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRU24191 786 bp
Trichoderma reesei beta-xylanase
U24191
U24191.1 GI:780815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (06-APR-1995) Willem H. van Zyl, University of
Stellenbosch, Microbiology, Victoria street, Stellenbosch,
South Africa
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    TCGGCTTTACCCCCGTTGCCCTTGCGGCCTTAGCCGCGACTGGGCCCTGGCCCTTCCCCGG
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                                                                                                                                                                       /gene="XYN2"
204. .773
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                                                                                                                                 /gene="XYN2"
/product="beta-xylanase"
                                                                                                                                                                                                                                                                                                                                                                                           /gene="XYN2"
/note="endo-beta-1,4-xylanase; endoxylanase"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="XYN2"
105. .776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Hypocrea jecorina"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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                                   Score 243.6; DB 15;
Pred. No. 4.9e-47;
0; Mismatches 249;
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X76047.1
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Humicola insolens
Humicola insolens
Eukaryota; Fungi; Ascomycota; mitosporic
1 (bases 1 to 1039)
Dalboege, H. and Hansen, H.P.H.
A novel method for efficient expression c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIXYL1 1039 bp mRN7 H.insolens XYL1 mRNA for endoglucanase.
                                                                                                                                                     Submitted (04-NOV-1993) H. Dalboege, Nordisk A/S, Symbion, Fruebjergvej 3,
                                                                                                                                                                                          Dalboege,H.
Direct Submission
                                                                                                                                                                                                                                                  Mol. Gen. Genet.
8190078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGGAATGCCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCACCTCCCTCGCCGGCGTCGCCGCCATCTCGGGCGTCTTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACGGCAGCGTCTACGACATTTACCGCACGCAGCGCGTCAACCAGCCGTCCATCATCGGCA 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCCGCTGGTCGAGTATTACATCGTCG 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTACCAGATTGTTGCCGTGGAGGGTTACTTTAGCTCTGGCTCTGCT
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                                      organism="Humicola insolens"

mol_type="mRNA"

db_xref="taxon:34413"

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                                                                                                                              ocation/Qualifiers
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165436
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                                                                                                                                             TGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCAT
                                                                                                                                                                   CTCGGTCAACATGCAGAACCACTTCAACGCGTGGCAGCAGCACGGAATGCCGCT---
                                                                                                                                                                             TACCGTCCAGACGGCTGCCACTTCGACGCCTGGCTCGCGCTGGTTTGAATGTCAACGG
                                                                                                                                                                                                                                                                          CGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACCTCGCGTCAACGCACCTAGCAT
                                                                                                                                                                                                                                                                                                      TGTCATCGAGTCGTACGGCACGTACAATCCCGGCAGCCAGGCTCAGTACAAGGGCACATT
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/EC number="3.2.1.8"
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/db_xref="InterPro:IPR008985"
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PSIDGTRTFQQYWSIRKNKRVGGSVNMQNHFNAWQQHGMPLGQHYYQVVATEGYQSSG
ESDIYVQTH"
47. .103
/gene="XYL1"
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              from
             patent
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Pred. No. 2.6e
0; Mismatches
            1123 bp
US 5667990
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.6e-46;
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RESULT 9
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Aspergillus express
BD006885
BD006885.1 GI:1863
JP 2001025393-A/2.
Humicola insolens
Humicola insolens
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Unclassified.
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1 (bases 1 to 1123)
Berka,R.Michael., Yoder,W., Takagi,
Aspergillus expression system
Patent: US 5667990-A 3 16-SEP-1997;
Location/Qualifiers
1. .1123
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Similarity 64.4%;
91; Conservative
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/mol_type="unassigned
GI:18635256
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Pred. No. 6.2e-
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Berka, R.M., Yoder, W., Takagi, S. and Boomi Aspergillus expression system Patent: JP 2001025393-A 2 30-JAN-2001;
NOVO NORDISK BIOTECH INC
OS Humicola insolens
PN JP 2001025393-A/2
PD 30-JAN-2000 JP 2000185449
PF 17-MAY-2000 JP 2000185449
PF C12R1-699 US 08/161675
PI CARAPPAN CHETYER BOOMINAZAN
PC C12N15/09, C12N1/15, C12N1/PC C12N15/09, C12N1/15, C12N1/PC C12N15/09, C12N1/15, C12N1/PC (C12N15/09, C12N1:66), (C12N15/00, C12N15/00, C12N15
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CCAGCACTACTACCA
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17-MAY-2000 JP 2000185449

01-DEC-1993 US 08/161675

RANDY M BERKA, WENDY YODER, SHINOBU TAKAGI,

CARAPPAN CHETYER BOOMINAZAN

C12N15/09, C12N1/15, C12P21/02//(C12N15/09, C12R1:66), (C12N15/09,

C12R1:685),

(C12N15/09, C12R1:69), (C12N1/15, C12R1:66), (C12P21/02, C12R1:66),

C12N15/00,
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:34413"
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Pred. No. 6.2e-46;
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  CCACCGAGGGCTACCAGAGCAGTGGCGAGTCCGACAT
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Trichoderma :
AY156910
AY156910.1
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Direct Submission

Submitted (30-SEP-2002) Forest and Environmental

University, 1 Hwayang-Dong, Kwangjin-Gu, Seoul 14

Location/Qualifiers
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Min,S.Y., Kim,B.G. and Ahn,J.-H.
Purification, Characterization,
Fungus Trichoderma Strain SY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trichoderma sp. SY
Trichoderma sp. SY
Trichoderma sp. SY
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 841)
Min,S.Y., Kim,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                                                                                                                                                                                                                                                      CAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACC
                                                                                                                                                                                                                                                                                                                                                   CTGGAACGACGGCCATGCCGGCGTGACTTACACCAACGGCGCTGGCGGGTCGTTCAGCGT 259
                                                                                                                                                                                                                                                                                                                                                                                                         GTGGAGTGACGGTGGAGCGCACGTACACCAACCTGGAAGGCGGCACCTACGAGAT 233
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                                                                                                                                                   AAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAAACAGCT
                                                                                                                                                                                                                           CAACTGGGCCAACTCGGGCAACTTTGTGGGAGGCAAGGGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTTGCGGCCTTAGCCGCGACTGGGGCCCTGGCCTTCCCGGCAGGGAATGCCACGGAGCT 113
    CGGCTGGTCCAAGAACCCGCTCATCGAGTACTACATTGTCGAGAACT
                                 CGGTTGGACCCCGAACCCCGCTGGTCGAGTATTACATCGTCGAGAACT
                                                                                                                 CAGAACCATCAACTTCTCCGGCAGCTACAGCCCCAACGACAACAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAAAAGCGTCAGGTCATTGGCCCCGGCACTGGCTTCAACAACGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="xylanase"
/protein_id="AAN78423.1"
/db_xref="GI:26514830"
/translation="MVAFTSLLAGFAAVAGVLSAPTEDVQVEKRQVIGPGTGFNNGYY
/translation="MVAFTSLLAGFAAVAGVLSAPTEDVQVEKRQVIGPGTGFNNGYY
YSYWNDGHAGVTYTNGAGGSFSVNWANSGNFVGGKGWNPGSSTRTINFSGSYSPNDNS
YLSVYGWSKNPLIEYYIVENFGTYNPSTGATKLGEVTLDGSVYDIYRTQRVNQPSIIG
TATFYQYWSVRRSHRSSGSVNVGNHFNAWRNLGLTLGQLDYQIIAVEGYFSSGSANIN
VS"
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/db xref="SY"
/db xref="taxon:215577"
60. .722
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 232.6; DB 15;
Pred. No. 2e-44;
0; Mismatches 264;
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3-701, South Korea
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                                                                                                                                                                                                                                                                                               CCGCCTGAACGC 293
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                                                                                                                       ACCTCTCCGTCTA
                                                                 TGGCACCTATGA 413
         TGGCACCTACAA 439
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Query Match 23.:
Best Local Similarity 60.0
Matches 393; Conservative
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Trichoderma viride s
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AY320048
AY320048.1 (
                                                                                                                                                                                                                                                                                                                            Direct Submission

Direct Submission

Submitted (10-JUN-2003) Key Laboratory of Industrial Microbiology & Fermentation Technology of Yunnan, School of Life Science, Yunnan University, 2 North Road, Green Lake, Kunming, Yunnan 650091, China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                Yang, Z.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang, Z.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cloning and characterization Trichoderma viride YNUCC0183
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1 (bases 1 to 672)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                 /organism="Trichoderma \
/mol_type="mRNA"
/strain="YNUCC0183"
/db_xref="taxon:5547"
1. .672
                                                                                                /EC number="3.2.1.8"
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GNSYLSVYGWSKNPLIBYYIVENFGTYNPSTGTTKLGEVTSDGSVYDIYRTQRVNQPS
IIGTATFYQYWSVRRNHRSSGSVTVANHFNAWRNLGLTLGTLDYQIIAVEGYFSSGNA
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                23.2%;
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Score 228.2; |
Pred. No. 2.2e
0; Mismatches
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   .2e-43;
es 253;
                                DB 15;
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                                 Length
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  Gaps
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                                                                 JOURNAL
PUBMED
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TITLE
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Fusarium oxysporum f
gene, complete cds.
AF246830
AF246830.1 GI:13491
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Fusarium oxysporum f. sp. lycopersici
Fusarium oxysporum f. sp. lycopersici
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Soro
                                                   Hera,C., Gomez-Gomez,E.
Direct Submission
Submitted (17-MAR-2000)
Cordoba, Avda. San Alber
                                                                                                                                                                                                                                  Hypocreomycetidae; Hypocreales; mitosporic Fusarium oxysporum complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATTGCCGTGGAGGGCTACTTTAGCTCTGGTAACGCCAACATTAACG
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pocreales; Fusarium;
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71, Spain
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protein (xyl5)
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ilarity 64.7%;
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/gene="xy15"
/codon_start=1
/product="xy1anase 5 protein"
/product="xy1anase 5 protein"
/protein_id="AAK27974.1"
/db_xref="GI:13491873"
/translation="MVHFTSVFAGLSLVAGSLAAPSKEGLFSKITKRAGTPNSSGTNN
GFYYSWWSDGGADATYTNGEGGGSYSMEWKDGGNVVGGKGWSPGKARTISYEGEYKPNG
NSYLSVYGWTRNPLVEYYIVESFGTYNPSSGATKKGTVEADGSTYDIFETTRTNAPSI
DGTQTFQQYWSVRQQHRSTGSVDTGLHFDAWEKAGMKLGTHDYQILATEGYFSSGSSH
MTVSEGASSGGGAGGSTGGDASQGGDSQQGGDASQGGNGQQGGNGFQQPG
SENQPQQQEIDTGANEPCQ"
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/db_xref="taxon:59765"
/note="forma_specialis:
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Submitted (10-NOV-1998) Avni A.,
University, Tel-Aviv University,
Location/Qualifiers
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Unpublished
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Trichoderma viride
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Trichoderma viride
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Soro
Hypocreomycetidae; Hypocreales; mitosporic Hypocre
Trichoderma; Tricoderma viride species complex.
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                                                                  CTCAGTCTATGGCTGGTCCAAGAACCCCCTCATCGAGTACTACATTC
                                                                                                                                CTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGGCTGGAACCCCCGG 284
                                                                                                                                                                                                                                                                   CTACTCCTACTGGAACGATGGCCATTCCGGCGTGACATACACCAACGGTGCTGGCGGCTC
                                                                                                                                                                                                                                                                                                                                    CGTGGACGTGGAGAAGCGCCAGACGATTGGCCCCCGGCACTGGCTTCAACAACGGCTACTA
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  AACCTACAACCCATCGACTGGCACCACCAAGCTGGGTGAGGTGACCT
                                  CACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCAT 464
                                                                                                 TGCGGTCTACGGTTGGACCCGCAACCCGCTGGTCGAGTATTACATCG
                                                                                                                                                                  CCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCT 344
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ilarity 56.8%;
Conservative
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IIGTATFYQYWSVRRNHAPAARSRLRTTSNAWRNLGLTLGTLDYQIIAVEGYFSSGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NINVS"
63. .161
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/product="endo-1,4-beta-xylanase"
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/db_xref="taxon:5547"
53__734
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Pred. No. 4.4e-40;
D; Mismatches 341;
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Tel-Aviv, 69978
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eales;
                                                                     TTGAGAACTTTGG
                                                                                                ICGAGAACTITGG
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                                                                                                     404
                                                                                                                                     382
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REFERENCE
AUTHORS
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PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
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                                                                                                                                                                                                                                                                                                                                                                                           The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from tanonica rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       740
2 (bases 1 to 912)
2 (bases 1 to 912)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Adachi, J., Aizawa, K., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, N., Hiramoto, K., Hiraoka, T., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, Y., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kanagawa, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
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FLI_CDNA; oligo capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                   japonica rice
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CDNA clone:002-168-G08,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                       365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.
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Direct Submission

Birect Submission

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head (Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yaz
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K.
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K.,
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GTGCAGTGGCGAACACTGGCAACTTCGTCGGTGGGAAGGGATGGAA
                                                                 ATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAAC
                                                                                                                                                                             TGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCCAACCTGGAAGGCCGGCACCTACGAG
                                                                                                                                                                                                                                                                         CTTGAGAGGCGCCAGTCCACCGCCAACTCAGTCGGAACTCACAACGGCTACTTTTACTCG 218
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 213; DB 15;
Pred. No. 9.4e-40;
); Mismatches 210;
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Yazaki,J.
Nami
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Shishiki, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                    <u>..</u>
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Hatsch,D., Phalip,V. a
Direct Submission
Submitted (09-JUN-2004
IFR 85 - ESBS -UIP, Bo
Illkirch-Graffenstaden
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Hatsch, D., Phalip, V. and Jeltsch, J.-M.
The xylanases of Gibberella zeae
Unpublished
(bases 1 --
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Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Hypocreomycetidae; Hypocreales; Nectriaceae;
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85 - ESBS -UIP, Boulevard Sebastien Brant - BP10413
circh-Graffenstaden, Alsace 67412, France
                                                                     /codon_start=1
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/translation="MVSF
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                                                                                GCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGA 643
                                                                                                                                   TCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCT 583
                                                                                                                                                              GCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCA 463
rcerrecaacegaegecracurcaecaecegerarecrecarcaece
                                                                                                           TCAACCAGTACTGGTCCATCCGCCGCAACAAGCGTACCAGCGGCTCC
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Search completed: | Job time : 5091.94 February 2006, 20

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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum
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80
  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 2000000000
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 100.0
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Match
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Gapop 10.0 , Gapext 1.0
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983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4996997 segs, 3332346308 residues
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geneseqn2000s:*
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(c) 1993
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  AAT40742
AAT43010
AAS13813
AAD17927
AAQ74098
AAQ94952
ABQ80364
AAZ28864
AAZ28864
AAZ28869
ADK70798
ADL23221
ADJ35015
AAT63044
AAX90405
AAT64930
AAV29598
ABQ80363
AAQ54775
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                                                                                                                                                                                                                       SUMMARIES
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10645.530 Million cell updates/sec
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Biocceleration Ltd
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Abq80362 A. fumiga Abq80364 A. fumiga Abq80364 A. fumiga Aaz28864 Streptomy Adz28865 Streptomy Add23221 A. niger Adj35015 DNA encod Aat63044 Aspergill Aax90405 Actinomad Aat64930 Actinomad Aav29598 DNA seque Abq80363 A. fumiga Aaq54775 T. reesei
                                                                                                                       Aat40742 Xylanase
Aat43010 Endo-1,4-
Aas13813 DNA encod
Aad17927 Thermomyc
Aaq74098 Humicola
Aaq94952 Humicola
                                                                                                                                                                                           Description
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AAT40742;

21-MAY-1997

(first entry)

AAT40742 standard; cDNA; 983 BP.

| Adj34943 DNA encod | ADJ34943 | 12 | 1041 | | 150.2 | 4 5 |
|--------------------|----------|----|------|------|-------|------------|
| Adj35017 DNA encod | ADJ35017 | 12 | 1071 | | 150.6 | 44 |
| Adj34999 DNA encod | ADJ34999 | 12 | 1065 | | • | 43 |
| Adl23220 A. niger | | 12 | 2439 | 15.6 | • | 42 |
| - | | 12 | 1047 | | 156.2 | 41 |
| Aaq69150 Aspergill | 7 | ຎ | 1581 | | 159 | 40 |
| - | ADJ34967 | 12 | 1083 | | 160.8 | 39 |
| _ | | 12 | 1044 | 16.4 | 160.8 | 38 |
| Adj35001 DNA encod | | 12 | 1083 | | 161.6 | 37 |
| | 20 | ຎ | 516 | 16.7 | 164 | 36 |
| Aaq74638 Aspergill | 5 | Ŋ | 927 | 16.8 | 165.2 | 35 |
| DNI | | 12 | 1299 | 16.8 | 165.4 | 34 |
| Þ | | 10 | 942 | | 165.4 | 33 |
| DNJ | ADJ35005 | 12 | 1044 | 16.8 | U | 32 |
| DNA | | 12 | 1041 | | 165.8 | 31 |
| Aaq36563 Endo-xyla | AAQ36563 | N | 675 | 17.1 | 168.4 | 30 |
| Adj35039 DNA encod | ADJ35039 | 12 | 1137 | | 170 | 29 |
| Adj34983 DNA encod | ADJ34983 | 12 | 1074 | | 170 | 28 |
| Aaq43458 Sequence | AAQ43458 | Ŋ | 572 | | 171.8 | 27 |
| Abq80361 A. fumiga | ABQ80361 | 10 | 712 | | 181.2 | 26 |
| | AAT71585 | N | 1281 | | 181.8 | 25 |
| Aaq03405 Streptomy | AAQ03405 | ผ | 1057 | | 183.4 | 24 |
| w | ADJ34949 | 12 | 1047 | | 185 | 23 |
| | ADJ35009 | 12 | 1059 | | 186.2 | 22 |
| Aaq90388 Xylanase | AAQ90388 | N | 1273 | 19.1 | 187.8 | 21 |
| | AAV81332 | N | 1015 | | 190 | 20 |
| | | | | | | |

ALIGNMENTS

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RESULT 1
AAT40742
XX
AAT40742
XX
AAT4
AC AAT4
XX
DT 21-M
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DE Xyla
XX
Chae
KW Chae
KW Byss
KW Plan
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FT CDS
FT C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermoascus; Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia; Byssochlamus; Paecilomyces; animal feed additive; in-vivo breakdown; plant cell wall; growth rate; feed conversion; ss.
                                          Claim
                                                                                                      Fungal xylanase prepns. construct for producing
                                                                                                                                                                                                                    WPI; 1996-454790/45
P-PSDB; AAW01112.
                                                                                                                                                                                                                                                                                                                                Hansen PK, Wagner P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermomyces lanuginosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xylanase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JAN-1995;
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                                       ٠<u>.</u>
                               Page 45-46; 69pp; English
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31. .708
/*tag= a
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/product= "xylanase"
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                                                                                                         for use as animal feed additives recombinant Thermomyces xylanase
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Best Local S
Matches 983
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                                                                                                   TGGTGATCTCGCGAGGCAACAGCCAAGAATGTCGTCAGATGTGCCGGTTGAAGGTATTCA
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 GAGCCTGGCCAGGATCAGTAGTTGCTTTTGCGGTGTTTTTGCTCCCTATTCTCGTGAAAAAA
                                                   ATCAGCATATCTGTCTGCCCTTGCGAGTGATACTTTGGAGGACTGTGGAGAACTTTGTGC
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Pred. No. 5.1e-255;
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RESULT 2
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                  The sequence encodes an endo-1,4-beta-D-xylanase from Thermomyces lanuginosus (Humicola lanuginosa), which may be used as a bread-improving additive. The enzyme may be expressed recombinantly from a plasmid pyES2.0 vector in Saccharomyces cerevisiae DSM 10133 (claimed), and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour, optionally along with other enzymes (amylase, maltogenase, lipase, cellulase, hemicellulase, pentosanase, glucose-oxidase, laccase, protease and/or peroxidase). The enzyme combines particularly well with amylolytic enzymes, and may be used to improve baking properties of flour and/or dough, by increasing volume and improving texture, flavour, crumb softness, freshness and anti-staling properties, while improving dough machinability and stability. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                              Bread improving additive alpha-amylase, increases
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Humicola lanuginosa; bread;
flour; baking; dough; ss.
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22-FEB-1997
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)B; AAW05187.
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                                                                                                          TGGTGATCTCGCGAGGCAACAGCCAAGAATGTCGTCAGATGTGCCGGTTGAAGGTATTCA
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           TGGTGATCTCGCGAGGCAACAGCCAAGAATGTCGTCAGATGTGCCGGTTGAAGGTATTCA
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Pred. No. 5.1e-255;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                 The invention relates to a variant xylanase polypeptide (I) or its CC fragment having xylanase activity, comprising one or more amino acid modifications such that (I) or its fragment has an altered sensitivity to CC a xylanase inhibitor as compared with the parent xylanase enzyme. (I) or CC its coding sequence (II) is useful for degrading or modifying plant cell CC wall or for processing a plant material by contacting the plant cell wall CC or plant material with (I) or (II). (I) is useful for modifying plant CC materials, and in baking, processing cereals, starch production, processing wood and enhancing the bleaching of wood pulp. (I) is useful CC for altering the viscosity derived from the presence of hemicellulose or crabinoxylan in a solution or system comprising plant cell wall material. CC (I) is useful for preparing a foodstuff such as bread, pretzels, cortillas, cakes, cookies, biscuits or crackers. The present sequence correseents the coding sequence of Thermomyces lanuginosus xylanase A as CC described in the method of the invention
                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 585; Conserv
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27-JUN-2000;
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                                                                                                                                                                                                                                                                                       Sequence
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GATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCGGCCTGAA
                                                                                         GGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAC
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2000GB-00015751.
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CACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGT

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The invention relates to a Pichia cell comprising at least one copy of heterologous nucleotide sequence encoding a polypeptide of interest, where the codon usage of the sequence has been adjusted to match the preferred codon usage of P. methanolica. The invention also relates to a method for producing high yields of heterologous codon optimised polypeptide in a Pichia cell. The Pichia cell is useful for producing a polypeptide of interest, where the polypeptide is encoded by a nucleotide sequence heterologous to P. methanolica. The present sequence is Thermomyces lanuginosus codon optimised xylanase gene which is the
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15-MAR-2000;
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27-AUG-2003
25-MAR-2003
14-NOV-1995
                                                            AAQ74098
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             Xylanase;
                       χY
                                                             standard;
             vector;
                       anase
                                (revised)
(revised)
(first entry)
             paxx40-1-1;
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                                                             DNA;
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              Aspergillus
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Humicola

insolens

foetidus;

SOXCCCCCCX PXXTTTXXRXX PXX PXXTTH

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Query Match
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Matches 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A DNA fragment (AAQ74098) encoding H. insolens xylanase (AAR75421) was isolated from pYES (DSM 6995) and inserted into pHD414 (contg. the TAI promoter and AMG terminator) to form pAXX40-1-1-1. This plasmid and pJaL77 (imparting hygromycin B resistance) were used to transform protoplasts of A. foetidus NO953. The xylanase yield was 0.12 g/l. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus foetidus cells expressing heterologous enzyme - partic. fungal lipase or xylanase, provide high yields without significant of protease or mycotoxin.
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P-PSDB; AAR75421.
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                                     CGACGGCACCCGGACGTTCCAGCAGTACTGGTCTATCCGCAAGAACAAGCGTGTCGGAGG
                                                        CGACGGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGG
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                                                                                                                                     TGTCATCGAGTCGTACGGCACGTACAATCCCCGGCAGCCAGGCTCAGTACAAGGGCACATT
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Query Match
Best Local Similarity
Matches 391; Conserv
                                                                                                                                                                                                                                                                             A strain of B. coli contg. the approx. 1,100 bp xylanase HindIII/ XbaI cDNA fragment in pYES is deposited in DSM as DSM 6995. The xylanase cDNA fragment is isolated from one of the clones. The sequence of the xylanase gene and protein are given in AAQ94952 and AAR78231 and the gene is deposited as DSM 6995. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-215271/28.
P-PSDB; AAR78231.
                                                                                                                                                                                                                                                                                                                                                                              Example; Page 39-40; 50pp;
                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus japonicus-type of tungal enzyme, provide high
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02-DEC-1995
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                                                                                CTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACAC 206
                                                                                                                 CGTTCCTCGGGACAACTCGÁCGGCCCTTCAGGCTCGÁCAGGTGÁCCC
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Pred. No. 5.4e-54;
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RESULT 7
ABQ80362
ID ABQ8
XX ABQ8
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P-PSDB; ABB80185.

Novel isolated Aspergillus fumigatus industries such as those involved in beverages, textiles and detergents. industries polypeptide, the making o in various and feed,

Page 163-64; 169pp; English.

The sequences given in ABQ80319-66 encode enzymatic proteins derived from CC A. fumigatus. The resulting proteins display the catalytic activity of an CC enzyme such as tannase, cellulase, glucose oxidase, glucosanylase, physiase, beta-galactosidases, invertase, lipase, alpha-amylase, laccase, polygalacturonase or xylanase. Compositions comprising the tannase are composition for modulating the amount of compounds that comprise a gallate seter linkage in a composition. Compositions comprising the compositions comprising the composition composition. Composition composition composition comprising the amount of composition. Compositions comprising the amount of for modulating the amount of myo-inositol phosphaces of majorate are useful for modulating the amount of for modulating the amount of myo-inositol phosphaces of modulating the amount of myo-inositol phosphaces or modulating the amount of myo-inosition. Compositions comprising lapae are useful for modulating the amount of compositions comprising the amount of myo-inositions comprising comprising alpha-amylases are useful for modulating the amount of oxidated phenolic compositions or maltodextrins in a composition. Compositions comprising comprising physalacturonases or useful for modulating the amount of oxidated phenolic compositions comprising polygalacturonases are useful for modulating the amount of oxidated phenolic compositions comprising polygalacturonases are useful for modulating the amount of oxidated phenolic compositions comprising polygalacturonases of a season and compositions comprising polygalacturonases of a composition compositions comprising polygalacturonases of a composition compositions comprising polygalacturonases of compositions comprising polygalacturonases of compositions compr

Sequence 999 BP; 142 A: 199 Ç 192 <u>ن</u> 133 T; ď; 0 Other;

Similarity

22.8%;

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666;

밁 Ś 밁 ঠ 밁 á 밁 Ś ঠ Query Match Best Local S Matches 413 121 61 91 3 ccgg---cagggaatgccacggagctcgaaaagcgacagacaacccccaactcggagggc ACGANTANCGGCTACTACTACTCCTTCTGGACCGACGGCGGCGGCCA TGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCA ATGGTCTCATTCTCTCTCGCTTCTCGCTGCCTCCACCGTTGCTGG ATGGTCGGCTTTACCCCCGTTGCCCCTTGCGGCCTTAGCCGCGACTGGGCCCCTGGCCTTC **AAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGG** AACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGA 267 CCCGGCTCGGAGCAATACGTTGAGCTAGCCAAGCGGCAGCTCACCAGCTCTCAGACTGGC **AACGGCAATGGCGGCCAGTATCAGGTCGACTGGAACAACTGCGGCAACTTTGTTGCTGGG** Conservative <u>,</u> Score 224.6; DB 10 Pred. No. 3.4e-50; 0; Mismatches 249; - AGCGAGAAAGCGGTCACCTACAGCGC Indels CTCCTGGCAGACC GGTGACCTACACC GGCCACGTACACC TGTTTACCAGCCA 327 CGTGCTAGCTACA 60 9; Gaps 297 180 207 120 240 147

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RESULT 8
ABQ80364
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                        Novel isolated Aspergillus fumigatus industries such as those involved in beverages, textiles and detergents.
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                                                    polypeptide, useful in
the making of food and
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Claim 2; Page 165-66; 169pp; English

Comprising sucrase or invertage are useful for modulating the amount of glyceride in a composition. Compositions comprising lipase are useful for comprising lipase are useful for modulating the amount of glyceride in a composition. Compositions of CC starches or maltodextrins in a composition. Compositions comprising CC laccase are useful for modulating the amount of oxidated phenolic care useful for modulating the amount of oxidated phenolic compounds in a composition. Composition comprising polygalacturonases CC are useful for modulating the amount of ingh or low molecular weight CC polygalacturonic acid chains in a composition. Compositions comprising CC xylanases are useful for modulating the amount of xylan or xylo-oligomers CC in a composition. The A. fumigatus proteins and corresponding DNA's are useful in various industries such as those involved in the making of food CC and feed, beverages, textiles and detergents. The DNA's are useful to express recombinant enzymes for characterization, modification or CC express recombinant enzymes for characterization, modification or to identify duplicated genes of paralogs having the same or similar CC biochemical activity and/or function, to compare with nucleic acid construction, to compare with nucleic acid construction, and to raise anti-protein antibodies. The polypeptide having CC tannase activity increases the yield of tea liquor from tea leaves, and to raise anti-protein antibodies. The polypeptide having CC improves the colour, flavour and health benefits of tea products, particularly an instant tea product. The polypeptide having cellulase activity enhances cleaning ability of detergent compositions useful for modulating the amount of compounds that comprise a year ester linkage in a composition. Compositions comprising cellulase are useful for modulating the amount of cellulose in a composition. Compositions comprising glucose oxidase are useful for modulating the amount of glucose or oxygen in a composition. Compositions comprising phytase are useful for modulating the amount of myo-inositol phosphates in a composition. Compositions comprising beta-galactosidases are useful for modulating the amount of lactose in a composition. Compositions comprising sucrase or invertase are useful for modulating the amount of compositions comprising the amount of lactose in a composition. polygalacturonase or xylanase. Compositions comprising the tannas useful for modulating the amount of compounds that comprise a call useful for modulating the amount of compounds that comprise a call useful for modulating the description. fumigatus. sequences given umigatus. The re ences given in ABQ80319-66 encode enzymatic proteins atus. The resulting proteins display the catalytic actus. The resulting proteins display the catalytic actus as tannase, cellulase, glucose oxidase, glucoamy beta-galactosidases, invertase, lipase, alpha-amylas the tannase are prise a gallate g cellulase are ns derived from activity of an laccase,

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Sequence 705 BP; 151 A; 227 C; 183 G; 144 T; 0 U; 0 Othe

Query Match Best Local

Similarity

22.7%;

Length

705;

Ś S 밁 ঠ 밁 ঠ B Ś 밁 밁 Ś 밁 S Matches 269 143 149 411; ဗ္ဗ GGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCCCAGGCCACGTACACCA 208 TGCTGGCGTGCTCCGCCATTGGAGCTCTGGCTGCCCCCGTCGAACCCGAGACCACCTCGT GTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGG AGGGCTGGAACCC **ATGGCGCCGGTGGCTCGTACTCCGTCAACTGGAGGAACGTGGGCAAC ACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAA** GGAACAACGGCTACTACTACTCCTTCTGGACTGATGGCGGCGGCGACGTGACCTACACCA rearestrosectra a construction de la construcción d **AGGGCTGGAACCCTGGAAGCGCTAGGTACCGAGCTTTAAGTÁGAACC** TCAATGAGACTGCTCTTCATGAGTTCGCTGAGCGCGCCGCCACCCCAAGCTCCACCGGCT Conservative <u>0</u> Score 223; DB 10; Pred. No. 9.4e-50;); Mismatches 250; CGGCCTGAACGCAAGAGCCATCCACTTTGAGG Indels TCCGGTGCTACCG ACCCGCAACCCGC ATCAACTACGGAG ACCACCAACCCCT 382 18; Gaps 373 322 148 313 262 268 202 142 82

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RESULT 9
AAZ28864
ID AAZ2
XX AAZ2
AC AAZ2
AC AAZ2
XX AAZ2
AC AAZ2
XX YJ1
DT 01-F
XX YJ1
XX YJ1
XX PT CDS
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P-PSDB;
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pulp-bleaching; ds
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01-FEB-2000
This sequence corresponds to a degenerate sequence encoding a precursor from Streptomyces olivaceoviridis. The sequence can into the plasmid pQE60 to generate plasmid FERM P-16713 for every. E.coli. The xylanase is useful for the preparation of xyl
                                                                                 A xylanase gene,
pulp-bleaching.
                                                                                                                                                                                                                                                                                                                                    sig_peptide
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                                                            Claim
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DB; AAY44183.
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/product= "xyl
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/*tag= b
418. .990
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/note=
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                        xylanase
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RESULT 10
AAZ28865
ID AAZ28
XX
AC AAZ28
XX
DT 27-AU
DT 01-FE
XX
DE Strep
XX
KW Xylan
KW pulp-
XX
FT CDS
FT CDS
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Best Loc
Matches
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2003 to correct
                                                                                                                   Xylanase; plasmid;
pulp-bleaching; ds.
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01-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                    GACAAGCGCACCAGCGGTACCCGTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCT 609
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                                                                                                                                                                                                                                      standard; DNA;
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nilarity 62.9%;
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OS field.)
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Pred. No. 8.5e-45;
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                                                                                                                                                                                                                                        ΒP
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                                                                                                                                  coli;
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                                                                                                                                  ride; xylan;
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SOXCCCCCX PX TTX RRX PX RX PX PX TT

additive;

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Query Match
Best Local S
Matches 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4;
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P-PSDB; AAY44183.
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SEIBUTSUKEI TOKUTEI SANGYO G:
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                                                                                                                                                                                                                                                                                                        GAGGGTGTTTACCAGCCAAACGGCAACAGCTACCGTTGCGGTCTACGGTTGGACCCCGCAAC
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                                                                                            GACAAGCGCACCAGCGGTACCGTCCAGACGGCTGCCACTTCGACGCCTGGGCTCGCGCT
                                                                                                                               TACAACGCCCCCCCGTGGAAGGCACCAAGACCTTCAACCAGTACTGGAGCGTCCGGCAG
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                                           GGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGC
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                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 353
                                                                                                                                                                                                                                                                                                                                         The present sequence encodes the Streptomyces olivaceoviridis xylan enzyme. The xylan enzyme has good heat stability, high activity under acidic and neutral pH. The xylan enzyme can be used as a feed additive and can be widely used in animal feed.
                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                      GAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAAC 369
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Pred. No. 1.7e-44;
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                                                                                    WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                             Aspergillus
                                                                                                                                                                                                                                                                                                                             ss; gene; A. niger; (hemi)cellulase; filament biscuit; elasticity; stability; stickiness; crumb structure; softness; flavour.
                                                                                                                                                                                                                                                                                                                                                                                                                    ADL23221
This sequence encodes an A. niger (hemi)cellulase NBE021. The (hemi)cellulase coding sequences of the invention are derived from a filamentous fungus, preferably Aspergillus niger. The (hemi)cellulase
                                                                                                                                                                                                                  15-AUG-2003;
                                                                                                                                                                                                                                                    WO2004018662-A2
                                                                                                                                                                                                                                                                                                                                                                                  20-MAY-2004
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                                   Disclosure;
                                                          Novel hemicellulase NBE012, NBE021, NBE022, derived from Aspergillus niger, useful for p
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                                                                                                                                                                                                                                                                                                                                                                 (hemi)cellulase NBE021 coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCATGCAACTGGGCAGCTTCAGCTACT
                                                                                                             Fritz A,
Boer DL,
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; 2002EP-00102160.
; 2002EP-00102161.
; 2002EP-00102245.
; 2002EP-00102279.
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                                                                                                                       Klugbauer
                                                                                                                                                                                                                                                                                                                                       filamentous fungus; dough; bread;
iness; extensibility; machinability;
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                                                                        ACCTTCAACTACATGATCGTTGCCACCGAGGGATACGAGAGCAGCGG
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                                                                                                                                                                                                                                                                                      The invention describes an isolated or recombinant polypeptide (I), having 50% or more identity to 190 300-1200 residue amino acid sequences (S1), given in the specification, over a region of 100 or more residues and the polypeptide as thermostable xylanase activity. (I) is useful for: dough conditioning; beverage production; as a nutritional supplement in animal feed; reducing lignin in a wood or a wood product; and for eliminating and protecting animals from a microorganism comprising xylan. The polynucleotide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylanase activity which involves amplification of a template nucleic acid with a primer pair capable of preventing bacterial infection and fungal infection e.g. coccidiosis. This sequence encodes xylanase protein isolated from an environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steer B, Callen Esteghlalian A;
                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                 Local Similarity
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)B; ADJ35016.
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Pred. No. 4.5e-44;
0; Mismatches 258;
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RESULT 14
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                                                                                                                                Identifying DNA fragments encoding proteins, e.g. discovery - by direct screening of a cDNA library with DNA from eukaryotic organism producing the pu
                                                                                                                                                                                                                         WPI; 1997-235889/21.
P-PSDB; AAW14597.
                                                                                                                                                                                                                                                                                       Van Den
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A cDNA clone (AAT63044), (AAW14597) of Aspergillus method for identifying a [

deposited as CBS 590.9 s niger N400 (CBS120.4) DNA fragment encoding

for a xylanase isolated using a of interest. The

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RESULT 15
AAX90405
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25-MAR-2003
28-SEP-1999
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                                                                                    processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               851 BP; 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCACGTACAAGGGCACCGTCACCTCGGACGGATCCGTTTACGATATCTACACGGCTACCC
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nilarity 61.3%;
Conservative
                                                                                                                                                                                                                                                      (revised)
(revised)
(first entry)
                                                                                                               sp. DSM43186; xylanase; Actinomadura
biobleaching; wood pulp; bleaching;
                                                                                                                                                                                               вp.
                                                                                                                                                                                                    DSM43186
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                                                                                         hemicellulose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 244 C; 224 G; 182 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGGGTACTCACAACTACCAGATCGTGGCTACCGAGGGTTACCAGA
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                                                                                       pulp;
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hemicellulase
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The present invention describes a culture medium obtained from the culture of a recombinant host cell that is not Actinomadura flexuosa and content into the manufacturity, where the protein comprises an amino acid sequence from a codifylic fragment of the amino acid sequence in AAY24481 or AAY24481.

CC Also described is an enzyme preparation derived from the culture medium. CC modifying plant biomass properties, especially the reduction of lignin content in pulp and paper processing. The xylanases are hemicellulases which partially degrade the hemicellulose and enhance the extractability content of wood pulp, increase its drainability or decrease its water retention. The culture medium can be used directly without the need to purify the enzymes. Actinomadura flexuosa xylanases have a ph optimum and content of acidify the pulp prior to xylanase treatment. The xylanases consent of lignin by conventional bleaching of wood pulp reducing the partially degrade the hemicellulose in wood pulp which enhances the consumption of bleaching chemicals reducing the partially degrade the hemicellulose.

CC partially degrade the hemicellulose in wood pulp which enhances the consumption of bleaching chemicals reducing the form lower consumption of bleaching chemicals reducing the form alower consumption of bleaching chemicals reducing the formation of continomadura sp. DSM43186 35 kDa xylanase N.B. This sequence is indexed consumption of streat as basic specification for F19503639.

CC Updated on 25-MAR-2003 to correct DR field.) (Updated on 16-OCT-2003 to
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Matches 403
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Maentylae A;
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31-OCT-1994;
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nilarity 58.6%;
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| 191.4 | • | - | 198.6 | • | 199.4 | 199.4 | 199.6 | 201.8 | 202 | • | 207.2 | 211.4 | 214.6 | 215.8 | 215.8 | 219 | • | • | 219.4 | 219.4 | 219.4 |
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| 682 | 746 | 746 | 871 | 738 | 677 | 655 | 746 | 673 | 697 | 671 | 714 | 921 | 708 | 770 | 711 | 734 | 763 | 729 | 916 | 891 | 886 |
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ALIGNMENTS

| | FEATURES source | TITLE JOURNAL COMMENT | ACCESSION VERSION KEYWORDS SOURCE ORGANISM | RESULT 1 DR637934 LOCUS DEFINITION |
|---|---|---|--|--|
| /organism="Gibberella moniliformis" /mol_type="mRNA" /strain="m3125" /db_xref="taxon:117187" /clone="FVMB275" /tissue_type="mycelia" /clone_Tib="FVM" /clone_Tib="FVM" | USDA 1815 N. University St, Peoria, IL 61604, USA Tel: 309 681 6230 Fax: 309 681 6689 Email: browndw@ncaur.usda.gov TIGR sequence name: FVMB275TH Seq primer: AAT TAA CCC TCA CTA AAG GG. Location/Qualifiers 1860 // Commonweight Commonstration of the commons of the common | Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y., Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A. Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005) Contact: Brown, D.W. | mycotina; Sordariomyceteriaceae; Gibberella. | DR637934 860 bp mRNA linear EST 11-JUL-2005 EST1028559 FvM Gibberella moniliformis cDNA clone FVMB275, mRNA |

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RESULT 2
DR643290
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sequence.

N DR643290

DR643290.1 GI:70718124

EST.

Gibberella moniliformis

Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

E 1 (bases 1 to 883)

E 1 (bases 1 to 883)

E 1 (bases 1 to 883)

S Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L, Lee, Y.,

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively

spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)

Contact: Brown, D.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102
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1815 N. University 9
Tel: 309 681 6230
Fax: 309 681 6689
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TIGR sequence name: FVMCX47TH
Seq primer: AAT TAA CCC TCA CT
Location/Qualifiers
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nilarity 67.4%;
Conservative
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/mol_type="mRNA"

/strain="m3125"

/db xref="taxon:117187"

/clone="FVMCX47"

/tissue_type="mycelia"

/clone Tib="FVMC"

/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;

/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;

/site 2: XhoI; anamorph: Fusarium verticillioIdes. Library

FvM was prepared from pooled RNA obtained from a 48-hour

and a 72 hour, liquid GYAM culture from strain M-3125.

Cultures were vacuum filtered and the mycelial mats were

frozen in liquid nitrogen, ground to a powder, and then

added to TRIzol Reagent (Invitrogen, Carlabad CA) at

approximately 1 g mycelia per 10 ml TRIzol. The cDNA was

directionally ligated into the pBlueScript II SK(+) XR

vector (cDNA Synthesis Kit; Stratagene)."
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Pred. No. 3.6e-71;
D; Mismatches 208;
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Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., De Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, Generation of ESTs from late blight-challenged potato tubers
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49478 5', mRNA sequence.
DR037502
DR037502.1 GI:66839397
EST.
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Contact: Barry Flinn
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                                                                                                                                             CACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAAGGCCAAGCCAAC
                                      AAGGCCGGTGGAGAGTACTCCCTGACCTGGAGCGGCAACGGCAACGTCGTTGCTGGAAAG
                                                                           CTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAG
                                                                                                                                                                                                           CCCGAGACCAGCCCTAACCCCCGCCACA----AGAAGCGCACGAACCAGACTGGCCAG
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/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum
absorption. The infection area was outlined for future
collection reference. Surface slices were sampled from the
tubers at 1 day, 5 days, 7 days, 11 days and 14 days
post-infection. All samples were pooled and used for RNA
isolation and library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996. Genome Research 6: 791-806)."
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/clone="49478"
/tissue_type="Tubers"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
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Pred. No. 1.1e-56;
); Mismatches 258;
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Flinn, B., Rothwell, C., Sardana, R., Griffiths, R.
Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pr
Generation of BSTs from late blight-challenged
Unpublished (2005)
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/tissue_type="Tubers"
/lab_host="XI10-Gold"
/clone_lib="Late_Blight-Challenged_Tubers"
/clone_lib="Late_Blight-Challenged_Tubers"
/note="Vector: pBluescript_II_SK(+) XR; Site_l: EcoRI;
/note="Vector: pBluescript_II_SK(+) XR; Site_l: EcoRI;
/note="Vector: pBluescript_II_SK(+) XR; Site_l: EcoRI;
/note="Total tubers war. Shepody, clone from pathogen-free Solanum tuberosum var. Shepody, clone 1756, were inoculated with 5 ul of Phytophthora infestans (A2-mating_type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum absorption. The infection area was outlined for future
                                                                                                                                                                                                                            /organism="Solanum tube
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="49478"
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Hypocrea jecorina (anamorph: Tr
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; P
Hypocreomycetidae; Hypocreales;
1 (bases 1 to 744)
Diener, S.B., Dunn-Coleman, N., F
Teunissen, P.J.M., van Solingen,
Ward, M. and Dean, R.A.
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                                                                                                                                                                                 CF867983

tric013xe09.b1 T.reesei mycelial culture,
Hypocrea jecorina cDNA clone tric013xe09,
CF867983
CF867983.1 GI:38122635
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.7%;
                                                                                         Ascomycota; Pezizomycotina; Hypocreales; Hypocreaceae;
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Pred. No. 8.9e-55;
0; Mismatches 251;
                          Solingen,
                                                                                                                                                               Trichoderma
                         Foreman,P., Houfek,
n,P., Dankmeyer,L.,
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Version 6 October
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primer: LT-F1 primer.
Location/Qualifiers
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/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric013xe09"
/dev_stage="mycelia"
/clone_lib="T.reesei myc
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Pred. No. 1.6e-53;
); Mismatches 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.3%;
Best Local Similarity 61.6%;
Matches 400; Conservative
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SM Hypocrea jecorina

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

E 1 (bases 1 to 799)

S Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
    451
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                                                                                                                                                                                                                                                                                                                                  211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, C
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-Fl primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       95
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                                                                           GGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCA
                                                                                                                                                                                                     AAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCT
                                                                                                                                                                                                                                                                                                                               AGGTCGAATCCGTGGCTGGAGAGCGCCAGACGATTCAGGCCGGCACGGCTACAACA
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   ACAGCTACCTCTCCGTGTACGGCTGGTCCCGCAACCCCCTGATCGAGTACTACATCGTCG
                        ACAGCTACCTTGCGGTCTACGGTTGGACCCCGCAACCCCGCTGGTCGAGTATTACATCGTCG
                                                                                                                                                                CCGGCGGCAGTTCTCCGTCAACTGGTCCAACTCGGGCAACTTTGTCGGCGGCAAGGGAT
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                                                                                                                                                                                                                                                                                     ATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAACCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric013xe09"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 3 april"
/note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."
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april Hypocrea
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510
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| | FEATURES source | , | TITLE JOURNAL COMMENT | REFERENCE AUTHORS | ACCESSION VERSION KEYWORDS SOURCE ORGANISM | RESULT 7 CN133022 LOCUS DEFINITION | Db 7 | n Ø | 0у 5 | Db 6 | ហ | 4 | Qy 3 |
|--|--------------------|---|---|--|--|------------------------------------|---|-----|---|---|---|---|--|
| /moltype="mRNA" /cultivar="BTx623" /cultivar="BTx623" /db_xref="taxon: 4558" /clone="OX1 9 D10 A002" /lab_host="DH10B-T1 phage-resistant B. coli" /clone_lib="Oxidatively-stressed leaves and roots" /clone_lib="Oxidatively-stressed leaves and roots" /note="Organ: Leaf and Root; Vector: pME18S-FL3; Site_1: /note="Organ: Leaf and roots were misted with loum methyl viologen. Leaves and roots were misted with 10 um methyl viologen. Leaves and roots were harvested at 3, 12 and 27 hr after treatment and all | , ne r | Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratt@uga.edu Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polva. | An EST database from Sorghum: oxidatively stressed leaves and roots Unpublished (2003) Other ESTs: OX1 9 D10.b1 A002 Contact: Cordonnier-Pratt MM | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum. 1 (bases 1 to 772) Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Cordonnier-Pratt, MM., Suzuki, Y., Sugano, S., C., Cordonnier-Pratt, MM., Suzuki, M. Su | DIO NOS 3, MEMA BEQUEIRE. | 772 bp mRNA linear | A RITACCAGATTGTTGCCGTGGGAGGGTTACTTTAGCTCTGGCTCTGCTC 796 | 91 | 75 AGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACT 634 | 15 CCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCC 574 | | 55 ACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCA | 395 AGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCG 454 |

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VERSION
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1 (bases 1 to 639)
Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, 1
Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,
Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR
                                                                                                                                                                                                                                                    sequence.
DR624928
                                                                                                                                               DR624928.1 GI:70699610
EST.
Gibberella moniliformis
Gibberella moniliformis
Gibberella moniliformis
Gibberella moniliformis
Gibberella moniliformis
Gibberella moniliformis
Hypocreamycetidae; Hypocreales; Nectriaceae;
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EST1015056
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larity 63.5%;
Conservative
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Pred. No. 1.1e-51;
D; Mismatches 209;
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                                                             GCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGA
                                                                                                                                    TCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCT
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      TCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTT 693
                                       CTATCTTCAATGCTTGGGCTAATGCTGGCATGAGACT--
                                                                                                     CCTATGATCTGTACCAGACCACCGCTACAACCAGCCCTCTATCGACGGCCAACAGACCT
                                                                                                                                                                                                                                                                                                       TCTGCGTCTACGGCTGGACCCGCAGCCCTCTCGTCGAGTACTACGTCATCGAGAACTACG
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CTTACAATCCCGGCTCTGCTGGCCAGCACAAGGGCACCGTCTACAACGACGGCGACA
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-TGGAAACCACTACTATCAGA

557 643 583

440 523 380 463

260 343

203

403

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USDA

1815 N. Univer

Tel: 309 681 6230

Fax: 309 681 6689

Email: browndw@ncaur.usda.gov

TIGR sequence name: FVIBB05TH

Seq primer: AAT TAA CCC TCA CTA AP

Location/Qualifiers

.639
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                           CCACGGAGCTCGAAAAGCGACGACGACCCCCAACTCGGAGGGCTGGCACGATGGTTATT 163
                                                                                          ACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACCGTACCTGGAAGGCGGCA 223
CCTACGAGATCAGCTGGGGAATGGCGGTAACCCTCGTCGGTGGAAAGGGCTGGAACCCCG
                                                                TCTACTCTTGGTGGTCTGATGGTGGTGGCTATGCCAACTACCGTATGGGTGAGGGAAGTC
                                                                                                                                                          CCTCTGTCCTTGAGGCCCGCCAGGTCACCGGTAACTCTGAGGGTTACCACAACGGATACT
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioIdes. Library
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10e6 conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIzol. The cDNA was
directionally ligated into the pBlueScript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="FVIBB05"
/tissue_type="mycelia"
/clone_Tib="FvI"
/note="Vector:_pBlueSc:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
                                                                                                                                                                                                                                                                            22.4%;
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Pred. No. 4.3e-
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3e-51;
8 211;
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                    283
                                                                  143
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GTCAACATGCAGA 590

ATCGAGAACTACG 410

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RESULT 9
DR623097
LOCUS
DEFINITION
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AUTHORS
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VERSION
KEYWORDS
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Best Local Similarity
Matches 373; Conserv
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Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIAM22TH
Seq primer: AAT TAA CCC TCA CTA AJ
Location/Qualifiers
1. .749
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Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, 1
Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,
Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
DR623097
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EST1013225
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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ACTACCAGGTTGATTGGCGCAACACTGGTAACTTTGTTGGTGGAAAGGGTTGGAACCCTG
                                        CCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCG
                                                                                                                        ACTATTCCTGGTGGAGTGACGGTGGAGCCCACGTACACCAACCTGGAAGGCCGCA
                                                                                                                                                                    CCTCTGTCCTTGAGGCCCGGCAGGTCACCGGTAACTCTGAGGGTTACCACAACGGATACT
                                                                                                                                                                                                            CCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATT
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                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                               /tissue_type="mycelia"
/clone_lib="FvI"
/clone_lib="FvI"
/clone_lib="FvI"
/note="Vector: pBlueScript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI; anamorph: Fusarium verticillioIdes. Library
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10e6 conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIzol. The cDNA was
directionally ligated into the pBlueScript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Gibberella moniliformis"
/mol_type="mRNA"
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FvI Gibberella moniliformis cDNA
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                                                                                                                                                                                                                                                                          22.4%;
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Pred. No. 4.5e-51;
); Mismatches 211;
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FVIAM22, mRNA
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293
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                                                                                                                                                                                                                                                                                           Email: ralph of Seq primer: L'
                                                                                                                                                                                                                                                                                                                                                        Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 270
Tel: 919-513-0020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; So:
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF881056 768 bp mRNA tric083xj11.b1 T.reesei mycelial culture, Hypocrea jecorina cDNA clone tric083xj11, CF881056 CF881056.1 GI:38135738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 768)
Diener, S.E., Dunn-C
Teunissen, P.J.M., v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Characterization of the protein processing and secretion pathways in a comprehensive set of expressed sequence tags from Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEMS Microbiol. Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diener, S.E., Dunn-Coleman, N., Foreman, P., Houfek, Teunissen, P.J.M., van Solingen, P., Dankmeyer, L., Ward, M. and Dean, R.A.
                                                                                                                                                                                                                                                                                                                                          Fax: 919-513-0024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTATCTTCAATGCTTGGGCTAATGCTGGCATGAGACT---TGGAAACCACTACTATCAGA 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTAGCTÁCCGAGGGATÁCCAGAGCAGTGGATCTTCTTCCATCTATGTT 697
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                                                                                                                                                                                                                                                                       il: ralph_dean@ncsu.edu
primer: LT-F1 primer.
Location/Qualifiers
                                    /note="Vector: pREP3Y; Site 1: Not I/Sal culture grown from 24 hrs to 6 days with
                  and Nitrogen sources and concentrations.
                                                                                  2003 11
                                                                                                                                                                                   /organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
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/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
                                                                                                                                                                  _xref="taxon:51453"
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Version 6 October 2003
mRNA sequence.
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T.D., Mitchell, T.K.,

I; Mycelial
varying Carbon

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RESULT 11
CB907827
                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                  REFERENCE
AUTHORS
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DEFINITION
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Best Loc
Matches
        JOURNAL
Hypocrea jecorina (anamorph: Trichoderma reesei)

SM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycet
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

E 1 (bases 1 to 822)
S Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in
filamentous fungus Trichoderma reesei
filamentous fungus Trichoderma reesei
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tric083xj11 T.reesei mycelial culture, Version 3 april Hypocrea jecorina cDNA clone tric083xj11, mRNA sequence.
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925 Page Mill Road, Palo Alto,

926 Page Mill Road, Palo Alto,

7el: (650) 846-7635

Fax: (650) 621-7817

Email: Pforeman@genencor.com

Seq primer: LT-F1 primer.
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/mol_type="mRNA"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric083xj11"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 3 april"
/note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."
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Best Local Similarity 63.2
372; Conservative
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DR624738.1
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Contact: Brown, D.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Kendra, D.F., Town, C.D. and Whitelaw, C.A. Analysis of 87,000 expressed sequence tags reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1815 N. University St,
Tel: 309 681 6230
Fax: 309 681 6689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gibberella moniliformis
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EST1014866
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GCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCCAGCCAAACGGCAACAGCTACCC
                                                                                                                                                                                                                                 CCTCTGTCCTTGAGGCCCGCCAGGTCACCGGTAACTCTGAGGGTTACCACAACGGATACT
                                                               ACTACCAGGTTGATTGGCGCAACACTGGTAACTTTGTTGGTGGAAAGGGTTGGAACCCTG
                                                                                         CCTACGAGATCAGCTGGGGAAGTGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCG
                                                                                                                                                 TCTACTCTTGGTGGTCTGATGGTGGTGGCTATGCCAACTACCGTATGGGTGAGGGAAGTC
                                                                                                                                                                                  ACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            il: browndw@ncaur.usda.gov
R sequence name: FVIBBOITH
primer: AAT TAA CCC TCA CTA
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                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="mycelia"
/clone Tib="FvI"
/clone Tib="FvI"
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioTdes. Library
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10e6 conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIzol. The cDNA was
directionally ligated into the pBlueScript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'db_xref="taxon:117187"
'clone="FVIB801"
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mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strain="m3125"
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                                                                                                                                                                                                                                                                                                                 Score 219.4; DB 8; Pred. No. 8.5e-51; 0; Mismatches 211;
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 719)

Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L, Lee Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D. Kendra,D.F., Town,C.D. and Whitelaw,C.A.

Nnalysis of 87,000 expressed sequence tags reveals alternativel spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)

Contact: Brown, D.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 309 681 6230

Fax: 309 681 6689

Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIEA21TH
Seq primer: AAT TAA CCC TCA CTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Brown, USDA/ARS/NCAUR
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/tissue type="mycelia"
/clone lib="FvI"
/clone lib="FvI"
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
/fvI was prepared from growth on excised maize seedling
/roots and shoots. The roots and shoots were then incubated by dipping briefly in
a suspension of 5 x 10e6 conidia per ml. The inoculated
/roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
/conditions for 4 days. Fungal mycelial was collected,
                                                                                                                                                                                                                                                                                                                                                       organism="Gibberella
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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'clone="FVIBA21"
                                                                                                                                                                                                                                                                                                                                      strain="m3125"
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RESULT 14
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Best Local S
Matches 372
                                                                                                                                                                                    ORGANISM
                                      JOURNAL
                                                                        TITLE
DR630899

ON EST1021027 FvI Gibberella moniliformis cDNA clone FVIDX40, mRNA sequence.

DR630899

DR630899.1 GI:70705629

EST.

Gibberella moniliformis

Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

E 1 (bases 1 to 733)

E 1 (bases 1 to 733)

E S Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L, Lee, Y.,

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively

spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)

Contact: Brown, D.W.

USDA/ARS/NCAUR
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Pred. No. 8.6e-51;
D; Mismatches 211;
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          TCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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USDA
1815 N. University St, Peoria, IL
1815 N. University St, Peoria, IL
Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIDX40TH
Seq primer: AAT TAA CCC TCA CTA A
/tissue type="mycelia"
/clone lib="FvI"
/clone lib="FvI"
/clone lib="FvI"
/clone lib="FvI"
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
/note = "Vector: pBlueScript II SK(+) XR
/clone | Ib="PVI"
/clone lib="PVI"
/clone
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/strain="m3125"
/db_xref="taxon:117187"
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CCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATT 22.3%; ; Score 219.4; DE; Pred. No. 8.6e-5 DB 8; e-51; 211; Length Indels ٠. 9 Gaps 163

ACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACCGTACACCTGGAAGGCGGCA 223 CCTACGAGATCAGCTGGGGAGATGGCGGTAACCCTCGTCGGTGGAAAGGGCTTGGAACCCCCG TCTACTCTTGGTGGTCTGATGGTGGTGGCTATGCCAACTACCGTATGGGTGAGGGAAGTC CCTCTGTCCTTGAGGCCCGGCCAGGTCACCGGTAACTCTGAGGGTTACCACAACGGATACT G---TACTGGCCGAACTATCAACTATGGCGGTTCTTTCAGCCCTCAGGGTAACGGCTATC GCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAAC ACTACCAGGTTGATTGGCGCAACACTGGTAACTTTGTTGGTGGAAAG **3GCAACAGCTACC** GTTGGAACCCTG 206 283 343 383 326 266

TTGCGGTCTACGGTTGGACCCGCAACCCCGCTGGTCGAGTATTACATCGTCGAGAACTTTTG TCTGCGTCTACGGCTGGACCCGCAGCCCTCTCGTCGAGTACTACGTC ATCGAGAACTACG 403 443

GCACTTACAATCCCGGCTCTGCTGGCCAGCACAAGGGCACCGTCTACAACGACGGCGACA GCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCA 463 503

CĊTATGATĊTGTAĊCAĠAĊCAĊCĊĠĊTAĊAAĊCAGĊCTCTATĊĠAĊĠĠCCAAĊAĠĀĊĊT TCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCT 563 523

GCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGA 643 TCAACCAGTACTGGGCCATCCGCCGCAACAAGCGCAGCAGCGGCGCTGTCAACATGCAGA 623 TCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCT TGGGAACCACTACTATCAGA 583 680

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ACCESSION
VERSION
KEYWORDS
SOURCE
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Best Local Similarity 63.3
Matches 372; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

ICE 1 (bases 1 to 739)
RS Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L, Lee,Y.,
Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR
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Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIB280TH
Seq primer: AAT TAA CCC TCA CTA AJ
Location/Qualifiers
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ACTACCAGGTTGATTGGCGCAACACTGGTAACTTTGTTGGTGGAAAGGGTTGGAACCCTG
                                          CCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCG 283
                                                                                                                                                                                CCTCTGTCCTTGAGGCCCGGCCAGGTCACCGGTAACTCTGAGGGTTACCACAACGGATACT
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//OCIONE_ILDETFYIT
//NOTES_TVECTOOT: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site_2: XhoI; anamorph: Fusarium verticillioIdes. Library
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10e6 conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIzol. The cDNA was
directionally ligated into the pBlueScript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Gibberella moniliformis"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:117187"
/clone="FVIB280"
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/clone_lib="FVI"
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Gibberella moniliformis
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                                                                                                                                                                                                                                                                      Score 219.4; DB 8;
Pred. No. 8.6e-51;
); Mismatches 211;
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mis cDNA clone FVIB280, mRNA
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                             TCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 692
                                                                                                  GCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGA 643
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Search completed: February 11, 2006, 20:39:40 Job time : 4981.03 secs

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US-08-458-023B-3
US-08-468-812-1
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US-08-290-979A-7
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| 8.4 | 8.4 | 8.4 | 8.4 | 8.6 | 9.6 | 9.7 | 9.8 | 9.9 | 9.9 | 10.0 | 10.0 | 10.3 | 10.5 | 10.5 | 11.1 | 11.1 | 12.1 | 12.1 | 12.1 | 12.6 | |
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| US-08-104-445-1 | US-08-104-445-2 | US-09-603-311-23 | US-09-390-234-23 | US-08-121-436A-3 | US-07-842-349-1 | US-09-260-283-1 | US-09-189-060B-46 | US-09-595-344-1 | US-08-315-695-15 | US-08-244-686-1 | US-07-955-726A-7 | US-09-367-891A-4 | US-09-613-811-5 | US-08-981-729-5 | US-08-963-500-2 | US-08-575-964-2 | US-09-189-060B-11 | US-09-970-616-1 | US-09-230-590-1 | US-09-462-246-1 | - |
| Sequence 1, Appli | Sequence 2, Appli | Sequence 23, Appl | Sequence 23, Appl | Sequence 3, Appli | Sequence 1, Appli | Sequence 1, Appli | Sequence 46, Appl | Sequence 1, Appli | Sequence 15, Appl | Sequence 1, Appli | Sequence 7, Appli | Sequence 4, Appli | Sequence 5, Appli | Sequence 5, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 11, Appl | Sequence 1, Appli | Sequence 1, Appli | Sequence 1, Appli | |

ALIGNMENTS

RESULT 1 US-08-886-765-1

Sequence 1, Application US/08886765 Patent No. 5817500

INFORMATION:

Kamp

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COUNTRY: USA
ZIP: 10174

ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324.204-US
REFERENCE/DOCKET NUMBER: 4324.204-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTILE TYPE: CONA
                                             MOLECULE TYPE: CORIGINAL SOURCE: ORGANISM: Theri
FEATURE:
NAME/KEY:
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TITLE OF INVENTION: Animal Feed
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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           AAAAAAAAAAAAAAAAAAAAAA
                                                                                     ACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCTTCGACCAATACTGGTCG
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                                                      TTGTTATTGCTTCGTTGTCTAGTGTACATAGCCGAGCAATTGAGGCCTCACGCTTGGGGAA
                                            TTGTTATTGCTTCGTTGTCTAGTGTACATAGCCGAGCAATTGAGGCCTCACGCTTGGGAA
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CURRENT APPLICATION

APPLICATION NUMBER: US/09/115,66

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/886,765

FILING DATE:

APPLICATION NUMBER: 08/886,765

FILING DATE:

APPLICATION NUMBER: 33,728

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 4324.

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 983 base pairs

TYPB: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

ORGANISM: Thermomyces lanugi
STRAIN: DSM 4109

FEATURE:

NAME/KEY: CDS

LOCATION: 31..705

US-09-115-660-1
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US-09-115-660-1
; Sequence 1, Application U; Patent No. 6245546
; Patent No. 6245546
; GENERAL INFORMATION:
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APPLICANT: Wagner, Peter
APPLICANT: Wagner, Peter
APPLICANT: Mullertz, Anette
APPLICANT: Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 62455460 No. 6245546disk
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
ADDLICATION NUMBER. IIS/00/115 660
                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 983; DB 3; Best Local Similarity 100.0%; Pred. No. 3.6e-269; Matches 983; Conservative 0; Mismatches 0;
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Hansen, F.
Hanser, Peter
: Wagner, Peter
/: Mullertz, Anette
/T: Knap, Inge Helmer
/T: Knap, Inge Helmer
/T'RNTION: Animal Feed A/
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                                                                                 CGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTA
                                                                                                                                                   GCCTTAGCCGCGACTGGGGCCTGGCCTTCCCGGCAGGGAATGCCACGGAGCTCGAAAAG 120
                 GACGGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGG 240
                                                                                                                                                                                                      TCGGCCCGACGTCTTGCAATCCTTGCAGTGATGGTCGGCTTTACCCC
                                                                                                                                     GCCTTAGCCGCGACTGGGGCCTGGCCTTCCCGGCAGGGAATGCCACGGAGCTCGAAAAG
GACGGTGGAGCGCAGGCCACGTACACCCAACCT
                                                                   CGÁCAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTA
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RESULT 3
US-08-458-023B-3
; Sequence 3, Application US/08458023B
; Patent No. 5667990
; GENERAL INFORMATION:
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                                                                           APPLICANT: Berka, Randy M.
APPLICANT: Yoder, Wendy
APPLICANT: Takagi, Shinobu
APPLICANT: Boominathan, Karuppan C.
TITLE OF INVENTION: ASPERGILLUS EXI
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56679900 No. 56679
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6201
COMPUTER READABLE FORM:
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EXPRESSION SYSTEM
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; NAME/KEY:
; LOCATION:
US-08-458-023B-3
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Best Local S
Matches 391
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Humicola insolens
INDIVIDUAL ISOLATE: DSM 6995
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Similarity 64.4%;
91; Conservative
                CTCGGTCAACATGCAGAACCACTTCAACGCGTGGCAGCAGCACGGAA
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126..806
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LOWNEY Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086.010-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1123 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: DNA (genomic)
TACCGTCCAGACGGCTGCCACTTCGACGCCTGGCCTCGCGCTGGTTTGAATGTCAACGG 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGACGGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGG 566
                                                                                                                                                                              CGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCA
                                                                                                                                                                                                                                                                          CATCGTCGAGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCG
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                                                                                                                                                                                                                                                                                                                                ccaggedaacegenacciegecerciaegeriggaecegeaaceege
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Pred. No. 1.1e-57;
D; Mismatches 210;
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                                                                                                                                                                                                                                                                                                                              TCGTCGAGTACTA 493
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RESULT 4
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; LOCATION:
US-08-468-812-1
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Patent No.
                                           Query Match 20.:
Best Local Similarity 58.0
Matches 403; Conservative
                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
APPLICANT: Kristo, Paula
TITLE OF INVENTION: Actinomad
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Larry B.
REGISTRATION NUMBER: 35,086
                                                                                                                                                                                                   FEATURE
                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 06-JU
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D.C.
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1100 New York Ave.,
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Lantto, Raija
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                                           Score 197.2; DB 2;
Pred. No. 9.1e-46;
D; Mismatches 273;
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application
Patent No. 6300114
GENERAL INFORMATION:
APPLICANT: M ntyl,
APPLICANT: Vehmaan
                                                                                                                                                                                                                        APPLICANT: Suominen, Pi
APPLICANT: Lahtinen, Ta
TITLE OF INVENTION: Pro
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                        ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                 STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                            COUNTRY:
                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                   T: Suominen, Pirkko
r: Lahtinen, Tarja
  INVENTION: Production
F SEQUENCES: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGGCGGCACCTACGAGATCAGCTGGGGGAATGGCGGTAACCTCGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08590563
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                                                                                                                                                                                  E: STERNE, KESSLER,
1100 New York Ave.,
                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                        Lantto, Raija
Paloheimo, Mar
                                                                                                                                                                                                                                                                                                                                                                                  Fagerstr m,
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      pc-Dos/Ms-Dos
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                                                                                                                                                                                                                                                                                                                                            Marja
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Richard
                                                                                                                                                                                    N.W. Suite 600
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LOCATION:
US-08-590-563-1
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REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 403; Conserv
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
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CCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCC
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06-JUN-1995
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Pred. No. 9.1e-46;
0; Mismatches 273;
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RESULT 6
US-09-770-621-1
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                                                                        TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                          CLASSIFICATION: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                 FILING DATE: 31-OCT-
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
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TITLE OF INVENTION: Pro
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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                         LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: No. 65065
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                TOPOLOGY:
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NVENTION: Production a
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1100 New York Ave.,
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M ntyl , Arja
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Paloheimo, Marja
Suominen, Pirkko
Lahtinen, Tarja
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US-09-770-621-1
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Best Local Similarity
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                                                            APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
                       APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                        INFORMATION:
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Pred. No. 9.1e-46;
0; Mismatches 273;
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Best Local Similarity
Matches 403; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: NO.
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
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CLASSIFICATION:
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DEDNESS: No. 6667170
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,832
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REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2600
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APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
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Pred. No. 9.1e-46;
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CAACACGGCGAAC 701

805 692 CACCTCCACCTTT 641

GACGCCAGCGTC

581

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GENERAL INFORMATION:

APPLICANT: WATANABE, MANABU

APPLICANT: WORIYA, TATSUKI

APPLICANT: MORIYA, TATSUKI

APPLICANT: SUMIDA, NAOMI

APPLICANT: SUMIDA, NAOMI

APPLICANT: MURAKAMI, TAKESHI

ITITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE cbh

ITITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR

ITITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH

FILE REFERENCE: 99-0266*/LC(wMC)/00144

CURRENT APPLICATION NUMBER: US/09/254,733

CURRENT APPLICATION NUMBER: US/09/254,733

CURRENT FILING DATE: 1999-05-07

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 8

LENGTH: 822

TYPE: DNA
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US-09-254-733-8
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US-09-254-733-8
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Patent No
                                                                             Query Match 19.8%;
Best Local Similarity 69.0%;
Matches 281; Conservative
                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
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NAME/KEY:
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NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: NAME/KEY: 819 peptide LOCATION: (14)...(112)
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ORGANISM: TRICHODERMA VIRIDE
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(14)..(112)
                                                                                                                                                                                                                                                                                                                                                   mat_peptide (113)..(809)
     CTGAAAACAAGGGTCATCAACTTCTCGGGCACCCTACAACCCCCAACGGCAACAGCTACCTC
                                        CTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTT
                                                                                                                                                                                                                                 intron
(286)..(412)
                                                                                                                                                                                                                                                                                           CDS
(113)..(285)
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                                                                          Score 194.2; DB 3;
Pred. No. 5.1e-45;
0; Mismatches 123;
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                                                                                                                 Length
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                                                                             Gaps
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US-08-121-436A-1
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Patent No
APPLICATION NUMBER: US 07/889,893
FILING DATE: 29-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,308
FILING DATE: 16-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.008000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, '

CURRENT APPLICATION DATA:
                                                                                                                                                                                                         APPLICATION NUMBER: US/08/
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI
APPLICATION NUMBER: PCT/FI
APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 24-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Saarelainen, Ritva
APPLICANT: Saarelainen, Ritva
APPLICANT: Paloheimo, Marja
APPLICANT: Lahtinen, Tarja
APPLICANT: Fagerstr m, Richard
TITLE OF INVENTION: No. 5837515el Enzyme Preparations
TITLE OF INVENTION: for Their Production
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Fox

and Methods

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Sequence 1, Application US/08768373
; Patent No. 6228629
; GENERAL INFORMATION:
APPLICANT: PALOHEIMO, MARJA
APPLICANT: HAKOLA, SATU
APPLICANT: WEHMAANPER, JARI
APPLICANT: LANTTO, RAIJA
APPLICANT: LANTTO, RAIJA
APPLICANT: LANTTO, RAIJA
APPLICANT: SUOMINEN, TARJA
APPLICANT: SUOMINEN, PIRKKO
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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US-08-768-373-1
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NAME/KEY:
LOCATION:
S-08-121-436A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
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COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
                                                                                                                                                  ADDRESSEE:
STREET: 11
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Local Similarity 68.5%;
Les 278; Conservative
                                                                                                                  CITY: WASHINGTON STATE: DC
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join(176..448,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 190; DB 2; I
Pred. No. 8.8e-44;
0; Mismatches 125;
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                                                                                                                                                    GOLDSTEIN &
   Version
                                                                                                                                                                                                                                      GENES
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FEATURE:
NAME/KEY: exon
LOCATION: 483..1039
OTHER INFORMATION:
US-08-768-373-1
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APPLICATION NUMBER: US 60/020,83
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 65.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DORIGINAL SOURCE: ORGANISM: Chae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: exon
LOCATION: 195..423
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN:
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                                                                                       TGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCAT 686
                                                                                                                           TACCGTCCAGACGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTT
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CAATGTTGGCGGC
                              CACCGTTGCTGAC
                                                             TTCCCATGATTATCAGATTGTGGCTACTGAGGGTTACTACTCGTCTG
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18-DEC-1995
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907
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Pred. No. 2.1e-41;
D; Mismatches 147;
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                                                              GCTCGGCGACTGT 894
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RESULT 11
US-09-849-242A-1
US-09-849-242A-1
Sequence 1, Application US/09849242A
Patent No. 6635464
GENERAL INFORMATION:
APPLICANT: PALOHEIMO, MARJA
HAKOLA, SATU
                                                                                           NAME/KEY: exon
LOCATION: 483..1039
OTHER INFORMATION: /F
SEQUENCE DESCRIPTION: SEQ
US-09-849-242A-1
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                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                    Matches
                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: US/09/849,242A
FILING DATE: 07-May-2001
CLASSIFICATION NUMBER: US 08/768,373
FILING DATE: 17-DEC-1996
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1716.0540004
TELEPHONE: (202) 371-2540
                                 / Match 18.5%;
Local Similarity 65.4%;
les 283; Conservative (
                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN &
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                             PEATURE:
267 ANAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCC 326
                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 195..423
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                   ORGANISM: Chaetomium thermophilum STRAIN: CBS730.95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: WASHINGTON STATE: DC
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OF INVENTION: NOVEL XYLANASES,
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LAHTINEN, TARJA
FAGERSTRTM, RICHARD
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VEHMAANPERO, JARI
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202) 371-2540
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                                                                                                                       /product= "}
EQ ID NO: 1:
                                                                                                                                                                                                              /product= "XLNA"
                               Score 181.8; DB 3;
Pred. No. 2.1e-41;
0; Mismatches 147;
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US-07-744-570B-1
                                                                                                           TOPOLOGY: US-07-744-570B-1
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                                                                                                                        FILING DATE: 19910813
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 675 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Single strand
TOPOLOGY: Circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/07744570B Patent No. 5202249 GENERAL INFORMATION:
                                               Query Match
Best Local Similarity
Matches 343; Conserv
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/7
FILING DATE: 19910813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kluepfel, D.
APPLICANT: Morosoli, R.
APPLICANT: Shareck, F.
TITLE OF INVENTION: Xylanase
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEB: Michael J. Bradley STREET: 1200 South 47th Street STREET: Box Number 4023 CITY: Richmond STATE: California
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               895
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127 ACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGT 186
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                                              Score 168.4; DB 2; Pred. No. 1e-37; ); Mismatches 211;
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                                               Indels
                                                                            Length
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                                                                            675;
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RESULT 13
US-08-507-431-5
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Patent No
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/507,431
FILING DATE: 15-FEB-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                       TITLE OF INVENTION: ENTITLE OF INVENTION: AS NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       STREET: 405 Lex
CITY: New York
STATE: New York
                                                                                                                                                      COUNTRY: United States ZIP: 10174-6401
                                                                                                                                                                                                                                           ADDRESSEE:
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Kauppinen, Markus S.
Christgau, Stephan
Heldt-Hansen, Hans !
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US-08-507-431-5
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US-08-902-655A-5
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Best Local Similarity
Matches 352; Conser
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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FEATURE:
NAME/KEY:
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REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3954.
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 60
FILING DATE: 25-AUG-1996
ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCT 226
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Pred. No. 9.4e-37;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,655A
FILING DATE: 30-July-1997
CLASSIFICATION: 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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LOCATION:
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TOPOLOGY: linear
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                                                                                                                                     TGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCC----AAACGGCAACAGCTAC
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Si, Joan Q.
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Christgau, Stephan
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RESULT 15
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APPLICANT: K
APPLICANT: K
               IBLEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                          STREET: 405 Lexington Avenue CITY: New York
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APPLICANT:
                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Agris, Cheryl H.
REGISTRATION NUMBER: 34,08
REFERENCE/DOCKET NUMBER: 3
TELECOMMUNICATION INFORMATION
                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,622
FILING DATE: 16-July-1998
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic STRANDEDNESS:
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/ENTION: ASPERGILLUS ACULEATUS
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; MOLECULE TYPE: DNA (;
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; NAME/KEY: CDS
; LOCATION: join(31.)
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0; Mismatches 248;
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Title: Perfect score: Sequence:

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Sequence 5, Appli
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Sequence 1, Appli
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Sequence 4, Appli
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Sequence 5, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 11, Appli
Sequence 6, Appli
Sequence 12, Appli

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications NA_Main:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USOOP_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USOOP_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USOOP_PUBCOMB.seq:*
                         100.0
38.0
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Match
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                         GenCore
(c) 1993
                                      US-09-467-368-1
US-10-237-386-9
US-09-803-454-3
US-10-425-115-177283
US-10-425-115-82922
US-10-425-115-37173
US-10-213-990-68
US-09-770-621-1
US-10-213-990-67
US-10-213-990-64
US-10-213-990-71
US-10-213-990-71
US-10-213-990-71
US-10-213-990-70
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Biocceleration Ltd.
                                  Sequence 1, Appli
Sequence 9, Appli
Sequence 3, Appli
Sequence 177283,
Sequence 82922, A
Sequence 65, Appl
Sequence 68, Appli
Sequence 1, Appli
Sequence 67, Appli
Sequence 71, Appl
Sequence 71, Appl
Sequence 21, Appli
Sequence 39, Appli
Sequence 8, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                             Description
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NUMBER OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US20020160080A1.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OSOFTWARR: PastSQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/467,368
FILLING DATE: 21-Dec-1999
CLASSIFICATION NUMBER: US/09/467,368
FILLING DATE: 21-Dec-1999
TASSIFICATION NUMBER: US/08/886,765
FILLING DATE: 1-UL-1997
ATTORNEY/AGENT INPORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3424.204-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: CDNA
ORGANISM: Thermomyces lanuginosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
US-09-467-368-1
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Patent No. US20020160080A1
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
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Wagner, Peter
Mullertz, Anette
Knap, Inge Helmer
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US-11-018-645-19

US-10-425-115-48309

US-10-626-583-4

US-10-437-963-15625

0 US-11-018-645-3

0 US-11-018-645-3

0 US-11-018-645-3

0 US-09-909-207-1

US-09-909-207-1

US-09-909-207-1

US-09-909-207-10

US-09-909-207-11

US-09-909-207-11

US-09-909-207-11

US-10-626-583-6

US-10-626-583-12

US-10-626-724-6

US-10-626-724-12

US-10-237-386-10
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US200201600

Regult No.

Score

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NAME/KEY: CDS

LOCATION: 31..70:
SEQUENCE DESCRIPTION:
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FEATURE:
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                                        GAGCCTGGCCAGGATCAGTAGTTGCTTTTGCGGTGTTTTTGCTCCCTATTCTCGTGAAAAAA
                                                                                                                      TGGTGATCTCGCGAGGCAACAGCCAAGAATGTCGTCAGATGTGCCGGTTGAAGGTATTCA
                                                                                                                                                              TACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGCTAAGACGTAACCTGG
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TTGTTATTGCTTCGTTGTCTAGTGTACATAGCCGAGCAATTGAGGCCTCACGCTTGGGAA
                                                                    ATCAGCATATCTGTCTGCCCTTGCGAGTGATACTTTGGAGGACTGTGGAGAACTTTGTGC
                                                                                ATCAGCATATCTGTCTGCCCTTGCGAGTGATACTTTGGAGGACTGTGGAGAACTTTGTGC
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APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO SEQ ID NOS: 66
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US-10-237-386
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; TYPE: DNA
; ORGANISM: Thermomyces
US-10-237-386-9
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Sequence 9, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 585; Conserv
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APPLICANT: Sibbese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTC
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                                                                                                                                                                                                                             CACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACC 363
                                                    CGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGCTGCCACTTCGACGCCTGGGCT 603
                                                                                                                              ACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCTTCGACCA
                                                                                                                                                                     GGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACC 483
 CGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGC
             CGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGC
                                                                                                             ACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCTTCGACCA
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AACGGAGGGCTAC 663
                                                                                                                                  ATACTGGTCGGTC 543
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APPLICANT: No. US20030022280Alozymes A/S
APPLICANT: Takagi, Shinobu
APPLICANT: Terui, Yuri
TITLE OF INVENTION: High Expression of Industrial En:
FILE REFERENCE: 6125.200-US
CURRENT APPLICATION NUMBER: US/09/803,454
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 52
SOPTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 678
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local S
Matches 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 72.0
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CACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACC
                                                                                                              GGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACC
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                                                         GTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGAC
                                                                                        GGTACTCAAACTTTCGATCAATATTGGTCTGTTAGACAAGATAAAAGAACTTCTGGTACT
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72.0%;
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Pred. No. 4.2e-109;
D; Mismatches 190;
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US-10-425-115-177283
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 177283
LENGTH: 850
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER
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                            GCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACC
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                                                                                                                                                                                                                                                                                                                                                         GCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCA 463
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                                                                                                                                                   TCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCC
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CCCACTTCGACGCCTGGGCCTCCAAGGGCATGCAGCT-
                                                                                                                                                                                                        CCTACAAGATTGCGCAGACTCAGCGTGTCAACCAGCCCTCCATCGAC
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RESULT 5
US-10-425-115-82922
; Sequence 82922, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 82922
LENGTH: 749
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Matches 423
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NAME/KEY: unsure
LOCATION: (1)..(749)
OTHER INFORMATION: 1
FEATURE:
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Similarity 63.9%;
23; Conservative
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Pred. No. 4e-68;
D; Mismatches 230;
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APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 37173

LENGTH: 818

TYPE: DNP
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US-10-425-115-37173
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Matches 411
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ORGANISM: Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                       CTCGTTCCTCCGGCGACCTCGTCGCTCGCCAGAGCACCCCCAACGCCGAAGGAACACACA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGGGAATGCCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACG 154
 CCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCC 574
                                                              ACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCA 514
                                                                                                                            AGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGA
                                                                                                                                                                                           ACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCGCTGGTCGAGTATTACATCGTCG 394
                                                                                                                                                                                                                                                                                                                                                                                     ATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAACCTGG 214
                                 ACGGCTCTTCCTACAAGATCGCTCAGTCGACCCGTACTAACCAGCC
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Pred. No. 4.1e-66;
D; Mismatches 241;
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                                TCCATCGATGGAA 572
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                                                                                               ACCGTGACTGCCG 512
                                                                                                                              ACTGTCGAGTGCG 454
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APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUM
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 666
TYPE: DNA
ORGANITOR:
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US-10-213-990-65
; Sequence 65, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
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Best Local S
Matches 413
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LOCATION: (1)...(666)
LO-213-990-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 413; Conser
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GAGAGCGACGGGCCACGTACAACCTCTACAAGACGACGCGGACGAATGCGCCGTCCATC
                         GAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATC 507
                                                                       ATCGTCGAGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTC
                                                                                                         AGCGGAAACGGCTACCTCTCCGTGTACGGCTGGACGACCAGTCCGCTGGTCGAATTCTAC
                                                                                                                         AACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCCGCAACCCCGCTGGTCGAGTATTAC
                                                                                                                                                                AAGGGCTGGAACCCGGCC---AGCGAGAAAGCGGTCACCTACAGCGGCTCCTGGCAGACC
                                                                                                                                                                                  AAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCA
                                                                                                                                                                                                                      AACGGCAATGGCGGCCAGTATCAGGTCGACTGGAACAACTGCGGCAACTTTGTTGCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACATGAAGACTCACTTCGATGCTTGGGCCAGCAAGGGCATGACTCT---TGGTAGCCACT 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACT 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTACCAGATTGTCGCTACCGAGGGATACTTCTCCACCGGTTCTGCGTCTATCACTGT
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larity 61.5%;
Conservative
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Pred. No. 4.5e-61;
); Mismatches 249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 666;
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; NAME/KEY: CDS
; LOCATION: (1)...(705)
US-10-213-990-68
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US-10-213-990-68
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Best Local Similarity
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TYPE: DNA
ORGANISM: Aspergillus
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Sequence 68, Application US/10213990

; Publication No. US20030082595A1

; GENERAL INFORMATION:

APPLICANT: Jiang, Bo
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry

TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENC
TITLE OF INVENTION: ENZYMES AND METHODS OF USE

FILE REFERENCE: 10182-019-999

; CURRENT APPLICATION NUMBER: US/10/213,990

; CURRENT FILING DATE: 2002-08-05

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTGGCGTGCTCCGCCATTGGAGCTCTGGCTGCCCCGTCGAACCCGAGACCACCTCGT 82
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                                                                                                       GCAGCTTCAACCCCAGCGCAATGGCTACCTGGCTGT
                                                                                                                                                          GTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGG
                                                                                                                                                                                                                                                                                                                                                      ACCTGGAAGGCCGGCACCTACGAGATCAGCTGGGGGAGATGGCGGTAACCTCGTCGGTGGAA 268
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TGATTGAGTACTACGTTGTTGAGTCGTATGGTACATACAACCCCGGC
                                                AGGGCTGGAACCCTGGAAGCGCTAGGTACCGAGCTTTAAGTAGAACC
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Pred. No. 1.5e-60;
); Mismatches 250
                                                                                                                                                                                                                                                                  CGGCCTGAACGCAAGAGCCATCCACTTTGAGG 313
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AGCGGCGGTÁCCT 442
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US-09-770-621-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09770621 Patent No. US20010024815A1 GENERAL INFORMATION:
TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: UFILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1100 New York Ave., N. CITY: Washington STATE: D.C. COUNTRY: U.S. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lahtiner
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                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                               APPLICATION NUMBER: US 08/282,001 FILING DATE: 29-JUL-1994
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Suominen, Pirkko
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Vehmaanper , Jari
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                                                                                                                                                                                             cccggacctriccagcagtrictiggagcgriccggcagcagaagcggaccagcgcaccarca 879
                             CTGACGTGGGCTAAGACGTAACCTGGTG
                                                                                 ACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCT
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Pred. No. 4e-52;
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; Sequential No. ; Publication No. ; GENERAL INFORMATION: ; APPLICANT: Mantyla, Arja; repricant: Paloheimo, Marja; repricant Paloheimo, Raija;

APPLICANT:
APPLICANT:

Lantto, Rai

Richard

APPLICANT:

Sequence 1, Application US/10286993 Publication No. US20030148453A1

RESULT 10

US-10-286-993-1

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/ LOCATION: (303)..(1337)
/ OTHER INFORMATION: Prod.
US-10-286-993-1
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APPLICANT: Vehmaanpera, Jari
TITLE OF INVENTION: Production and Secretior
TITLE OF INVENTION: Fungi
FILE REFERENCE: 1716.0340004
CURRENT APPLICATION NUMBER: US/10/286,993
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/120,804
PRIOR APPLICATION NUMBER: PCT/F197/00037
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1997-01-24
PRIOR APPLICATION NUMBER: US 08/590,563
PRIOR APPLICATION NUMBER: US 08/590,563
PRIOR PILING DATE: 1996-01-26
NUMBER OF SEQ ID NOS: 18
SOPTWARE: PatentIn version 3.0
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Best Local
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LENGTH: 1375
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ORGANISM: Actinomadura
FEATURE:
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Local Similarity 58.6%;
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                                                                         AGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACT
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); Mismatches 273;
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US-10-213-990-67
; Sequence 67, Application US/102:
; Publication No. US20030082595A1
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Local Similarity 57.8%;
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                                                                                                                                                                                                                                                                                                                                                      AGGGCTGGAACCCCGGCCTG---
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENC
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 67
LENGTH: 739
TYPE: DNA
ORGANISM: Aspergillus
US-10-213-990-67
GGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCA 208
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                                                                                                                         AGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCAT(
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                                                                                                                                                                                                                                                                                                                                       TTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAATGAGACTGCTCTTCATGAGTTCGCTGAGCGCGCCGGCACCCCAAGCTCCACCGGCT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCCGGCAGGGAATGCCACGGAGGCTCGAAAAAGCGACAACCCCCCAACTCGGAGGGCT 148
                                                                                ACCTTCACCCAGTACTGGTCTGTGCGCACCTCCAAGCGTACCGGCGG
                                                                                                                                                                                      GĠĊĀCTTĀCAACATĊTĀĊĀCĠGĊĊGTTĊĠĊTĀĊĀĀTĠĊTĊĊCTCĊĀT
                                                                                                                                                                                                                                                                                                                                                                                                                                              TACCTTGCGGTCTACGGTTGGACCCGCAACCCGCTGGTCGAGTATTACATCGTCGAGAAC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGGCTGACAGAAGTAGAACCATCAACTACGGAGGCAGCTTCAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGCTGGAACCCTGGAAGCGCTAGGTACCGAGCTTTGTCAACGTCGGATGTGCAGACCT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGCGCCGGTGGCTCGTACTCCGTCAACTGGAGGAACGTGGGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATGGTCGGCTTTACCCCCGTTGCCCCTTGCGGCCTTAGCCGCGACT
                                                                                                                                                                                                                                                                                           TATGGTACATACAACCCCGGCAGCGGCGGTACCTTCAGGGGCACTGT
                                                                                                                                                                                                                                                                                                                                                                                                ACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 190.6; DB Pred. No. 4e-50; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249;
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    TGACCACTACTAC 639
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|CAACACCGACGGT 502
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                                                                                CÁCTGTCACCATG 622
                                                                                                                                                                                                                                                                                                                                           CGAGTGCGACGGT 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCGGCAATGGC 382
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APPLICANT: Jiang, Bo
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUR
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64
LENGTH: 712
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US-10-213-990-64
; Sequence 64, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
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Best Local Similarity 57.7%;
Matches 412; Conservative
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                                                                                                 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGTCGGCTTTACCCCCGTTGCCCCTTGCCGCCTTAGCCGCGACTGGGGGCCCTGGCCTTC
                                                                                 CTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCTT
                                                                                                                                  CTCCTATGACCCCTCCACGGGAGCCACCCATCTCGGCACCGTCGAGAGGCGACGGGGCCAC
                                                                                                                                                          CACCTATGATCCTTCCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCAT
                                                                                                                                                                                                     CTCCGTGTACGGCTGGACGACCAGTCCGCTGGTCGAATTCTACATCGTGGAGAGTTACGG
                                                                                                                                                                                                                        TGCGGTCTACGGTTGGACCCCGCAACCCCGCTGGTCGAGTATTACATCGTCGAGAACTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                      AACCTGGAAGGCGCACCTACGAGATCAGCTGGGGGAGATGGCGGTAACCTCGTCGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGAATAACGGCTACTACTACTTCTTGGACCGACGGCGGCCAGGTGACCTACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCGGCTCGGAGCAATACGTTGAGCTAGCCAAGCGGCAGCTCACCAGCTCTCAGACTGGC
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                                                                 gracaaccreracaagacgacgacgaargcargcccarccarccagggcacggcracrrr
                                                                                                                                                                                                                                                                         TAATGGATTCAGAGCGGTCACCTACAGCGGCTCCTGGCAGACCAGCGGAAACGGCTACCT
                                                                                                                                                                                                                                                                                                                                            AAGGGCTGGAACCCGGCCAGCGAGAAGTATGCGTCCTCCCCTGCTTGTTAGGTTCAAGC
                                                                                                                                                                                                                                                                                                                                                                            AAGGGCTGGAACCCCGGCCTGAACGCA-----
                                                                                                                                                                                                                                                                                                                                                                                                              AACGGCAATGGCGGCCAGTATCAGGTCGACTGGAACAACTGCGGCAACTTTGTTGCTGGG
TGACCAGTACTGGTCGGTTCGGACTTCGCACCGGCAGAGTGGAACTGTGACGACGAAGAA
                         CGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGGCGGTACCGTCCAGACGGGCTG
                                                                                                                                                                                                                                                                                                        --- AGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCT
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Pred. No. 4.1e-47;
D; Mismatches 253;
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APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGI.
TITLE OF INVENTION: ENZYMES AND METHODS OF
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 71
LENGTH: 942
TYPE: DNA
ORGANISM: Aspergillus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(942)
US-10-213-990-71
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US-10-213-990-71
; Sequence 71, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
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Best Local S
Matches 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACC.
                                                                                                                             GACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCTTCGACCAATACTGGTC 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTTGCGACGGAGGGTACCAGAGCAGCGGCTCTGCTACTATCACTG
                                                                                GGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCCACTTTCGACGCCTG 599
                                                                                                                                                                                                                                                                                     GACCCGCAACCCGCTGGTCGAGTATTACATCGTCGAGAACTTTGGCACCTATGATCCTTC 419
                                                                                                                                                                                                                                                                                                                                      CATTACCTTCTCTGGCAGCTTCAATCCTTCCGGAAATGCTTACCTGTCCGTGTATGGATG 335
                                                                                                                                                                                                                                                                                                                                                           CATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTG 359
                                                                                                                                                                                                                                                                                                                                                                                                         CCAGAACGGTGGTGACTTTACCTGTGGGAAGGGCTGGAATCCAGG---GAGTGACCATGA 275
                                                                                                                                                                                                                                                                                                                                                                                                                               --GAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCGGCCTGAACGCAAGAGC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGA
                           GGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGG 659
                                                               CATCCGCCAAAACAAGCGATCCAGCGGCACAGTCACCACCGCGAATC
                                                                                                                                                                                                                                                                     GACTACCAACCCCTAGTCGAATACTACATCCTCGAGAACTATGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCGGATCAGTGCAATATACAAATGGTGCTGGTGGCGAATATAGTGTGACGTGGGCGAA 218
                                                                                                                                                                                                    CTCGGGCATGACGCACAAGGGCACCGTCACCAGCGATGGATCCACCTACGACATCTATGA 455
                                                                                                                                                                                                                                   16.8%;
nilarity 59.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 165.4; DB 5;
Pred. No. 5.6e-42;
0; Mismatches 221;
CCTGGGTACCCA
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                                                               ACTTCAAGGCCTG
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TTTCCACTGAGGG
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                                                                 575
 632
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APPLICANT: Bedford, Michael
APPLICANT: Pulliam, Derrick
TITLE OF INVENTION: Microbially Expressed Xy
TITLE OF INVENTION: Uses
FILE REFERENCE: 70357WOPCT
CURRENT APPLICATION NUMBER: US/11/018,645
CURRENT FILING DATE: 2004-12-20
PRIOR APPLICATION NUMBER: 60/531,404
PRIOR FILING DATE: 2003-12-19
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.2
SEQ ID NO 21
LENGTH: 978
TYPE: DNA
ORGANISM: Artificial Sequence
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LOCATION: (1)..(978)
US-11-018-645-21
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Publication No. US20050208178A1
GENERAL INFORMATION:
APPLICANT: Bauer, Michael
APPLICANT: Bedford, Michael
APPLICANT: Pulliam, Derrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.8%;
Best Local Similarity 56.8%;
Matches 327; Conservative
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OTHER INFORMATION:
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                                                             TCGAAGCGCGTGGGCGCACCATCACCATCGCCAACCATT
                                                                                                                                                                                                                          ACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGC
                                                                                                                                                                                                                                                                                                                                           GAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAAC
                                                                                                                                                                                                                                                                                                                                                                                        AACAACTGGGTGGGCGAAGGGCTGGGCTACCGGCTCCAGCCACACGATCAGCTACTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGTCGAGCCAGACGGCACCAACAACGGCAATTACTTTTCGTTCTGGAAAGACAGTCCG
                      GGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGC
                                                                                            GACAAGCGCACCAGCGGTACCGTCCAGACGGCTGCCACTTCGACGCCTGGGCTCGCGCT
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                                                                                                                            GTGAACCAGCCATCCATCATCGCCAACGCCACGTTCTACCAGTACTGGAGCGTGCGGCAG
                                                                                                                                                         GGCACGTTCAATTCGCCG----GGCAACGGTTACCTGGCCCTGTATGGCTGGACCACCAAT
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  - CCTGGGCCAGCAACTACCAGGTCATGGCCACCGAGGGTTACCAGAGC
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Pred. No. 1.1e-38;
0; Mismatches 243;
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RESULT 15
US-10-213-990-70
US-10-213-990-70
; Sequence 70, Applicat
; Publication No. US200
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUN
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 70
LENGTH: 1002
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Best Local Similarity
Matches 249; Conserv
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                                  CGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT
                                                                                                      ACGCCTGGGCTCGCCTGGTTTGAATGTCAACGGTGACCACTACTACC
                                                                                                                                                                                                                                                                                                                             ATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGAC 472
                                                                                                                                                                                                                                                                                                                                                                  ATGGATGGACTACCAACCCCTAGTCGAATACTACATCCTCGAGAACTATGGCAGTTACA 448
                                                                                                                                                                                                                                                                                                                                                                                            ACGGTTGGACCCGCAACCCCGCTGGTCGAGTATTACATCGTCGAGAACT
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CTGAGGGATATGAGAGCAGCGGTACCTCGACCATCACTGT
                                                                                                                                            ACTGGTCCATCCGCCAAAACAAGCGATCCAGCGGCACAGTCACCACC
                                                                                                                                                                               ACTEGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCCACTTCG 592
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                                                                       AGGCCTGGGCTAGTCTGGGGATGAA---CCTGGGTACCCATAACTATC
                                                                                                                                                                                                                                                                                           ATCCTGGCTCGGGCATGACGCACAAGGGCACCGTCACCAGCGATGGATCCACCTACGACA 508
                                                                                                                                                                                                                      TCTATGAGCACCAACAGGTCAACCAGCCTTCGATCGTCGGCACGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCGGCAGCTCCGACATCACCGTGACCGAAGGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10213990
No. US20030082595A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 4.1e-36;
); Mismatches 148;
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                                                                     PAGATTGTTTCCA 685
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                                                                                                          AGATCGTTGCAA 652
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                                                                                                                                                                                                                    CCTTCAACCAAT 568
                                                                                                                                                                                                                                                      CCTTCGACCAAT 532
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earch completed: February 11, 2006, 23:51:27 ob time : 1025.32 secs

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).

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Run

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Minimum DB
Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  186.2
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2812.856 Million cell updates/sec
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   59.5
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: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

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1: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1 US-11-170-653-9
US-10-517-939-231
1 US-11-108-1638-1
1 US-11-108-1638-3
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US-10-517-939-165
US-10-517-939-169
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Sequence 9, Appli
Sequence 231, App
Sequence 1, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 255, App
Sequence 255, App
Sequence 251, App
Sequence 271, App
Sequence 195, App
Sequence 195, App
Sequence 217, App
Sequence 218, App
Sequence 253, App
Sequence 215, App
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US-11-170-653-9
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Result

| 45 | 44 | 43 | 42 | 41 | 40 | <u>.</u> 9 | 38 | 37 | 36 | <u>3</u> 5 | υ 4 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 |
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| 89.8 | 90.2 | 91 | 91 | 91.4 | 91.8 | 92.4 | 93.4 | 94.2 | 95.4 | 106.8 | 107.2 | 108.4 | 109.2 | 114.8 | 116.4 | 118 | 119.2 | 124 | 127.8 | 128 | 131.2 | 141.8 | 146.4 |
| 9.1 | 9.2 | 9.3 | 9.3 | 9.3 | 9.3 | 9.4 | 9.5 | 9.6 | 9.7 | 10.9 | 10.9 | 11.0 | 11.1 | 11.7 | 11.8 | 12.0 | 12.1 | 12.6 | 13.0 | 13.0 | 13.3 | 14.4 | 14.9 |
| 1077 | 570 | 1053 | 645 | 678 | 570 | 1338 | 1068 | 570 | 1983 | 555 | 636 | 633 | 1020 | 1068 | 1086 | 669 | 642 | 1695 | 747 | 1029 | 1047 | 1077 | 1047 |
| 7 | | | | | | | 7 | | | | | | | | 7 | 7 | \vdash | | 7 | | | | 7 |
| US-10-517-939-369 | US-10-517-939-375 | US-10-517-939-191 | US-10-517-939-157 | US-10-517-939-171 | US-10-517-939-377 | US-10-517-939-367 | US-10-517-939-163 | US-10-517-939-189 | US-10-517-939-353 | US-10-517-939-251 | US-10-517-939-197 | US-10-517-939-207 | US-10-517-939-153 | US-10-517-939-205 | US-10-517-939-211 | US-10-517-939-167 | US-11-214-413-31 | US-10-517-939-317 | US-10-517-939-227 | US-10-517-939-219 | US-10-517-939-161 | US-10-517-939-181 | US-10-517-939-299 |
| Sequence 369, | Sequence 375, | | Sequence 157, | | Sequence 377, | Sequence 367, | Sequence 163, | Sequence 189, | | | | | | Sequence 205, | Sequence 211, | Sequence 167, | Œ | Sequence 317, | Sequence 227, | Sequence 219, | Sequence 161, | Sequence 181, | Sequence 299, |
| App | Appl | App | App | App | App | App | App |

ALIGNMENTS

```
Sequence 9, Application US/11170653;
Publication No. US20050271769A1;
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Alt
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23;
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 588
; TYPE: DNA
; ORGANISM: Thermomyces lanuginosus
US-11-170-653-9
                                                                                                                                                                                                                                                           Query Match 59.5
Best Local Similarity 100.
Matches 585; Conservative
                                                                                                                                                                       64
                                                                                                        GGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGA 243
                                      GATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCGGCCTGAA
                                                                                                                                                                                                                                                               59.5%; Score 585; DB 11; 100.0%; Pred. No. 1.9e-148; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Altered Sensitivity to Xylanase Inhibitor
                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                            588;
                                         CGCAAGAGCCATC 303
GCAAGAGCCATC 183
                                                                                       ATCAGCTGGGGA 123
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APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR FILING DATE: 2003-06-16
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 231
LENGTH: 1008
TYPE: DNA
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US-10-517-939-231
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                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Bacteria
US-10-517-939-231
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                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 386; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Wu, Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304
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                                                                                   ACAACCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGT
                                                                                                                                                     GCCGCGACTGGGGCCTGGCCTTCCCCGGCAGGGAATGCCACGGAGCTCGAAAAAGCGACAG
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                                                                                                                                                                                              20.6%;
ilarity 59.1%;
Conservative
                                                                                                                                                                                              Score 202.2; DB 7;
Pred. No. 5.7e-45;
0; Mismatches 258;
                                                                                                                                                                                                                             Length 1008;
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Sequence 1, Application US/11108163B; Publication No. US20060014247A1; GENERAL INFORMATION:

APPLICANT: Paloheimo, Marja
APPLICANT: Mantyla, Arja
APPLICANT: Heskinen, Sanna
APPLICANT: Fagerstrom, Richard
APPLICANT: Fagerstrom, Richard
APPLICANT: Puranen, Terhi
APPLICANT: Suominen, Pirkko
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: Method and DNA Constructs for Incre
TITLE OF INVENTION: Carbohydrate Degrading Enzymes in
FILE REFERENCE: 1716.034000B/MAC/DJN
CURRENT APPLICATION NUMBER: US/11/108,163B
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US 60/562,692
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
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US-11-108-163B-1
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OTHER INFORMATION: Nf xynllA nucleotide sequence (AJ508952), the coding region is
OTHER INFORMATION: from nt 303 to nt 1337
US-11-108-163B-1
                                                                                                                                           Query Match
Best Local Similarity
Matches 403; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Nonomuraea
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                                                                     TCGGCTTTACCCCCGTTGCCCTTGCGGCCTTAGCCGCGACTGGGCCCTGGCCTTCCCGG 94
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ilarity 58.6%;
Conservative
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                                                                                                                                           Score 197.2; DB 11;
Pred. No. 1.4e-43;
0; Mismatches 273;
  AÍCGCCGGTGCGC 408
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                                                                    APPLICANT: Puranen, Terhi
APPLICANT: Lantto, Raij
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level
TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
FILE REPERENCE: 1716.034000B/MAC/DJN
CURRENT APPLICATION NUMBER: US/11/108,163B
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US 60/562,692
PRIOR APPLICATION NUMBER: US 60/562,692
PRIOR PILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.3
SEQ ID NO 5
LENGTH: 663
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APPLICANT:
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                                                           LENGTH: 66
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FEATURE:
                                           ORGANISM: Nonomuraea
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INFORMATION:
ANT: Paloheimo, Marja
ANT: Mantyla, Arja
ANT: Mantyla, Arja
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Kallio, Jarno
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RESULT 5
US-11-108-163B-4
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Sequence 4, Application US/11108163B Publication No. US20060014247A1 GENERAL INFORMATION:
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Pred. No. 8.6e-42;
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; APPLICANT: Paloheimo, Marja
; APPLICANT: Mantyla, Arja
; APPLICANT: Leskinen, Sanna
; APPLICANT: Leskinen, Sanna
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Kallio, Jarno
; APPLICANT: Kallio, Jarno
; APPLICANT: Suominen, Terhi
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
; TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
; TITLE OF INVENTION CARBOHYDRAC/DJN
; CURRENT APPLICATION NUMBER: US/11/108,163B
; CURRENT APPLICATION NUMBER: US/11/108,163B
; CURRENT APPLICATION NUMBER: US 60/562,692
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 906
; TYPE: DNA
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APPLICANT: Paloheimo, Marja
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APPLICANT:
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OTHER INFORMATION: am3
OTHER INFORMATION: Exa
OTHER INFORMATION: sec
                                APPLICANT: Puranen, Terhi
APPLICANT: Lantto, Raij
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production
TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
FILE REFERENCE: 1716.034000B/MAC/DJN
CURRENT APPLICATION NUMBER: US/11/108,163B
CURRENT FILING DATE: 2005-04-18
CURRENT FILING DATE: 2005-04-18
                                                                                                                                        APPLICANT:
PRIOR APPLICATION NUMBER: US 60/562,692 PRIOR FILING DATE: 2004-04-16 NUMBER OF SEQ ID NOS: 25
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                                                                                                                                       Leskinen, Sanna
Fagerstrom, Rich
Kallio, Jarno
Puranen, Terhi
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llarity 61.2%;
Conservative
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Pred. No. 9.6e-42;
0; Mismatches 218;
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; OTHER INFORMATION: US-11-108-163B-3
RESULT 7
US-11-108-163B-2
; Sequence 2, Application US/11108163B
; Publication No. US20060014247A1
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Best Local Similarity
Matches 361; Conser
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TYPE: DNA
ORGANISM: Nonomuraea i
FEATURE:
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Pred. No. 6.3e-41;
); Mismatches 220;
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GENERAL INFORMATION:

APPLICANT: Paloheimo, Marja
APPLICANT: Heskinen, Sanna
APPLICANT: Leskinen, Sanna
APPLICANT: Fagerstrom, Richard
APPLICANT: Kallio, Jarno
APPLICANT: Wantio, Jarno
APPLICANT: Puranen, Terhi
APPLICANT: Lantto, Raij
APPLICANT: Suominen, Pirko
TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
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TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
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Sequence 225, Application US/10517939

Publication No. US20060003433A1

GENERAL INFORMATION:

APPLICANT: Steer, Brian

APPLICANT: Callen, Walter

APPLICANT: Healey, Shaun

APPLICANT: Hazlewood, Geoff

APPLICANT: Blum, David

APPLICANT: Esteghlalian, Alireza

TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS

FILE REFERENCE: 564462007901

CURRENT APPLICATION NUMBER: US/10/517,939
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US-10-517-939-225
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; OTHER INFORMATION:
US-11-108-163B-2
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2
LENGTH: 906
TYPE: DNA
ORGANISM: Nonomuraea flexuosa
FEATURE:
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Best Local Similarity 60.9%;
Matches 361; Conservative
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Pred. No. 7e-41;
D; Mismatches 2
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US-10-517-939-165
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 GENERAL INFORMATION
APPLICANT: Steer, I
APPLICANT: Callen
APPLICANT: Healey
APPLICANT: Hazlew
APPLICANT: Wu, Di
APPLICANT: Blum, I
APPLICANT: Estegh
TITLE OF INVENTION
                                                                                                                    Sequence 165, Application US/10 Publication No. US20060003433A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
 f: Blum, David
f: Esteghlalian, Alireza
INVENTION: XYLANASES, NU
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Callen, Walter Healey, Shaun Hazlewood, Geoff Wu, Di

NUCLEIC

ACIDS ENCODING

Brian

US/10517939

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PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 225
LENGTH: 1059
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                                                                                                                                    CAGAAGCGGACCGGCAGCATCACCACCGGCAATCACTTCGACGCCTGGGCCGCATAC 564
                                                                                                                                                            GACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCCACTTCGACGCCTGGGGCTCGCGCT 609
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AGCGGCTATGCTCGCATCACCGTTGCTGACGTGGG
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Pred. No. 1.2e-40;
); Mismatches 223
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                                               GGTTACCAGAGC
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RESULT 10
US-10-517-939-199
'; Sequence 199, Applica
; Publication No. US200
; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 165
LENGTH: 1047
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Best Local S
Matches 340
APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geof
APPLICANT: Wu, Di
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ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: (
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Local Similarity 60.6%;
les 340; Conservative
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                                                                                                       Application US/10517939 to. US20060003433A1
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Pred. No. 2.6e-40;
); Mismatches 215;
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APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENG
TITLE OF INVENTION: AND METHODS FOR MAKING AND
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 199
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TYPE: DNA
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                                                                                                                                                                                                                                                         TCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCTTCGACCAAT 532
                                                                                                                                                                                                                                                                                                  ATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGAC 472
                                                                                                                                                                                                                                                                                                                                                                                                ACGGTTGGACCCGCAACCCCGCTGGTCGAGTATTACATCGTCGAGAAC
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                             CGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT
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CCGAGGGCTACCAGAGCAGCGGCAGCTCCGACATCACGGT
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                                                                                                                                                                                   ACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCCACTTCG 592
                                                                                                                                                                                                                          TCTATCGCACGCAACGGGTCAACCAGCCGTCGATCATCGGCACCGCGACGTTCTACCAGT 502
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57.5%;
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                                                                           ACCAGGTGATGGCCA 619
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RESULT 11 US-10-517-939-255

Sequence

255,

Application

US/10517939

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TYPE: DNA
CORGANISM: Unknown
FEATURE:
COTHER INFORMATION: COUS-10-517-939-255
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APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENC
TITLE OF INVENTION: AND METHODS FOR MAKING AND
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 255
LENGTH: 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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CGGAGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 692
                                                                                                           ACTGGAGCGTGCGGCAGTCGAAGCGCACCGGCGCATCACCACGGCCAACCACTTCA
                                                                                                                                                                                                                                                         GTCCGCCGGGTGGCCAGGGCTTCATGGGCACGGTGAACACCGACGGCGCGCACGTACGACA
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                                     ATGCCTGGGCCAGCCTCGGCATGAA----CCTGGGACAGCACAACTACCAGGTGATGGCCA
                                                                       ACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAA
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Healey, Shaun
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nilarity 57.5%;
Conservative
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Pred. No. 3e-36;
0; Mismatches 260
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AND USING
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APPLICANT: ESTEGHIBLIAN, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR PILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 169
LENGTH: 1041
TYPE: DNA
ORGANISM: Unknown
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US-10-517-939-169
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Best Local Similarity
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ACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGGCACCTACGAGATCAGCTGGGGGAGATGGCCGGTAACCTCGTCGGTGGAAAAGGGCTGG 276
                                                                   GCCACGTTCTACCAGTACTGGAGCGTGCGGCAGTCGAAGCGCGTCGG
                                                                                                    CAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGC
                                                                                                                                                                                                                                                                                                                 GGCTATCTCACCTTGTACGGATGGACCACGAATCCATTGATCGAGTA
                                                                                                                                                                                                                                                                                                                                                                                                CAGACGGGCTCCAACCGCACGGTGACCTACTCC---GGTTCGTTCAATTCGCCCCGGCAAT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                           AACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAAC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCAACTACTTTCCTTCTGGAAGGACAGCCCGGGTACCGTCAACTTCTGCATGTATGCC 171
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Healey, Shaun
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Pred. No. 3.9e-
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CGTCAACAGCGAT 408
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                                                                                                     CGTACCGTCCAG 576
   CGGTGACCACTAC 636
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                                                                                                                                                                                          ATCGACGGCACC 516
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                                                                  GGCACGATCACC 528
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APPLICANT: Esteghlalian, Alireza
APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE
CURRENT APPLICATION: AND METHODS FOR MAKING AND USING THE
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 221
LENGTH: 1044
TYPE: DNA
ORGANISM: Unknown
PEATURE:
OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-221
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US-10-517-939-221
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APPLICANT: Callen, Walte
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Ge
APPLICANT: Wu, Di
APPLICANT: Blum, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 221, Application US/10517939 Publication No. US20060003433A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                      GTGTTTACCAGCCAAACGCCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACCAGGTCATGGCCACCGAGGGTTACCAGAGCAGTGGCAGCTCCGACATCACCGTGACC 645
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                                                                                                                                                                                                                                                                                                                                       CGGTGACCTTCTGCATGTATGCCAACGGCCGCTACACCTCCAACTGGAGCGGCATCAACA
                                                                                                                                                                                                                                                                                                                                                                        AGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTA
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                                                                                               ATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCA
                                                                                                                                                        CGTTCAACTCGCC---
                                                                                                                                                                                                                                                                    ACTGGGTGGGTGGCAAGGGCTGGCAGACCGGTCGAATCGCACGGTGACCTACTCCGGTT
                                                                                                                                                                                                                                                                                                     ACCTCGTCGGTGGAAAGGGCTGGAACCCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGG
 ACCAGCCTTCCATCATCGGCACCGCGACGTTCTACCAGTACTGGAGCGTGCGGCAGTCGA
                                                                  Hazlewood, Geoff
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Healey, Shaun
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larity 58.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 165.6; DB 7;
Pred. No. 4.5e-35;
D; Mismatches 234;
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 505
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APPLICANT: Blum, David

APPLICANT: Esteghlalian, Alireza

TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THE

TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE

FILE REFERENCE: 564462007901

CURRENT APPLICATION NUMBER: US/10/517,939

CURRENT FILING DATE: 2004-12-13

PRIOR APPLICATION NUMBER: PCT/US03/19153

PRIOR FILING DATE: 2003-06-16

PRIOR APPLICATION NUMBER: 60/389,299

PRIOR APPLICATION NUMBER: 60/389,299

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 380

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 177

LENGTH: 1299

TYPE: DNA

ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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US-10-517-939-177
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Best Local Similarity 56.3%;
Matches 351; Conservative
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Healey, Shaun
Hazlewood, Geof
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                                                          GAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAAC 369
                                                                                                            AACAACTGGGTTGGCGGTAAAGGCTGGATGCCGGG---TACTCGGCGCACAGTCACCTAT 264
                                                                                                                                                                                                                           GCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGC 249
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                                                                                                                                      GGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCGGCCTGAACGCAAGAGCCATCCACTTT 309
                                                                                                                                                                                                                                                                  AGCTCAAATGCCACTGGAACCCAGAATGGTTACTACTATTCGTTTTGGAAGGATTCCGGT 147
                                                                                                                                                                                                                                                                                              ACCCCCAACTCGGAGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGA 189
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 CCGCTGGTCGAGTATTACATCGTCGAGAACTTTGGCACCTATGATCC
                                        TCGGGCAGTTATAGCGCGAGTGGAACCAGCTACCTCGCACTTTACGC
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o. US20060003433A1
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 165.4; DB 7;
Pred. No. 5.5e-35;
D; Mismatches 266;
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  TTCCTCCGGTGCT 429
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APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
ITITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS
ITITLE OF INVENTION: AND METHODS FOR MAKING
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR FILING DATE: 2003-06-16
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 217
LENGTH: 1083
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US-10-517-939-217
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APPLICANT: Steer, Brian APPLICANT: Callen, Walte APPLICANT: Healey, Shaur
                                                                                                                                                                                                                                                                                                  Query Match 16.4%;
Best Local Similarity 56.8%;
Matches 359; Conservative
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
 370
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GGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCGGCCTGAACGCAAGAGCCATCCACTTT
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                                                              GAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAAC
                                                                                                 AACAACTGGGTCGGCGGCAAGGGCTGGTCGACCGGCTCCAGC---CGCACCGTCAGCTAT
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                                TCGGGCAGCTTCAATTCGCCCGGCAACGGCTACCTGACTCTCTACGGGTGGACCACCAAC
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Healey, Shaun
Hazlewood, Geoff
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o. US20060003433A1
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DS FOR MAKING AND USING
                                                                                                                                                                                                                                                                                                  Score 161.6; DB 7;
Pred. No. 5.4e-34;
); Mismatches 264;
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AGCAGCAACGGCGGCAGCAGCAATGGCGGCAG
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ALIGNMENTS

RESULT 1
AR044575
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Best Local Similarity 100
Matches 675; Conservative source M Unknown.
Unclassified.
3 1 (bases 1 to 983)
S Hansen, P.Kamp., Wagner, P., Mullertz, A. ar Animal feed additives
Location/Qualifiers
983 181 151 121 211 91 61 31 AR044575 Sequence 1 AR044575 AR044575.1 Unknown. CTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCT CACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCC CCGGCAGGGAATGCCACGGAGCTCGAAAAGCGACAGACAACCCCCCAACTCGGAGGGCTGG 150 ATGGTCGGCTTTACCCCCCGTTGCCCTTGCGGCCTTAGCCGCGACTGG ATGGTCGGCTTTACCCCCGTTGCCCTTGCGGCCTTAGCCGCGACTGGC GGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAAC 300 CACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCC CCGGCAGGGAATGCCACGGAGCTCGAAAAGCGACAGACAACCCCCCAACTCGGAGGGCTGG 120 /organism="unknown" /mol_type="unassigned from patent GI:5966040 100.0%; Score 675; DB 6; 100.0%; Pred. No. 4.8e-130; tive 0; Mismatches 0; 983 bp US 5817500. DNA" DNA and Length Knap, Indels linear 983; .Helmer. GTCGGTGGAAAG 270 SCCCIGGCCITC 90 GTCGGTGGAAAG 240 ACGTACACCAAC 180 CGTACACCAAC 210 PAT 29-SEP-1999

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RESULT 2
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Xylanase variants having altered sensitivity
Patent: WO 0166711-A 9 13-SEP-2001;
DANISCO A/S (DK)
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Eukaryota; Fungi; Ascomycota;
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                                                                                                 GGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGA
                                                                                                              GGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGA
                                                                                                                                               CAGACAACCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGAC 63
    CACTTTGAGGGTGTTTACCAGCCAAACGGCAACA
                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .588
                                                                                                                                                                                                                                                    /organism="Thermomyces
/mol_type="unassigned |
/db_xref="taxon:5541"
                                                                                                                                                                                                                                                                                                                                                                                                                                              588 bp from Patent W00166711.
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                                                                                                                                                                                             Score 582; DB Pred. No. 1e-0; Mismatches
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                             CTACGGTTGGACC 333
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Schlacher, A., Holzmann, K., Hayn, M., Steiner, W. and Schwab, H. Cloning and characterization of the gene for the thermostable xylanase XynA from Thermomyces lanuginosus
J. Biotechnol. 49 (1-3), 211-218 (1996)
8879171
2 (bases 1 to 2460)
Schlacher, A., Holzmann, K., Hayn, M., Steiner, W. and Schwab, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene, comp
U35436
U35436.1
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Submitted (06-SEP-1995) Institute
Biocatalysis, TU-Graz, Petersgasse
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Thermomyces lanuginosus
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota;
1 (bases 1 to 2460)
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Thermomyces lanuginosus
gene, complete cds.
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/note="putative"
/note="putative"
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join(1065 ..1330,1437 ..1848)
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969. .976
                                                                                                                                                                                                              /organism="Thermomyces lanuginosus"
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860. .2106
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Location/Qualifiers
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Local Similarity 86.4%;
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Pred. No. 5.6e-106;
D; Mismatches 0;
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CTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCCAAACCTT 494
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                                              CGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGG 674
                                                                                                                                               CCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGAT 614
                                                                                                                                                                                                                                                                                                   CTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACG
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/note="determined by homology"
2106
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GTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYAR
ITVADVG"
1065. .1157
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Direct Submission
Submitted (26-NOV-2003) MIPS, Institut fuer Bioinformatik,
GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH,
Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail:
G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute
of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf,
E-mail: ulrich-schulte@uni-duesseldorf.de
BAC clone 10D6 (strain OR74A) is available at the Fungal Genetic
Stock Center, http://www.fgsc.net
Sequencing was performed by MWG Biotech AG, Ebersberg, Germany,
http://www.mwgdna.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Information on performance of analysis and a annotation of this entry and other sequences http://mips.gsf.de/proj/neurospora.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurospora
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                                                                                                                                                                                                                                                                                                                                                                                           complement (join(232..1210,1265..1881,1942..2121))
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/gene="B1
complement (1882.
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                                                                                                                                                                                                                                                                                                               WYRLDEADNALMMTQGEYEDLLAWFDSYKEVKQEVKLPPPVVLVTDEEGNEFLAEEDD MSFATTQHGTVETQDSASEAITITD" complement (232. . .1210)
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crassa DNA linkage g
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Nyakatura, G.,
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                                                           .1941)
                                                                                                                                           .1881)
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I BAC clone B10D6.
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Neurospora.
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complement (join (4810. .
/gene="B10D6.030"
complement (join (4810. .
/gene="B10D6.030"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (3033. ./gene="B10D6.020" /number=1
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FDVLHSPSPKKRLTRRYFNPQSRPPFPPATTARGISFNTRTPLRNTTATKTDDHLADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (4810. .5445)
/gene="B10D6.030"
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/gene="B10D6.020"
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/gene="B10D6.020"
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AEERNRILSAIW"
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/gene="B10D6.030"
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complement (join (6522. .7140,7180./gene="B10D6.040"
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/number-~
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Query Match
Best Local Similarity
Matches 418; Conser
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GTGGAGTGACGGTGGAGCGCACGCACGTACACCCAACCTGGAAGGCGGCACCTACGAGAT
                                                               CGCCGAGCGTGGCGGTACCCCAGCAGCAGCACCGGCTTCAACAACGGCTTCTACTACTACTCCTT
                                                                                                                                                 cciccrcéececrécéereccrcécrarécccrrcaaceccacceaerrcreaecr
                                                                                                     CGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTG
                                                                                                                                                                                         CCTTGCGGCCTTAGCCGCGACTGGGCCTGGCCTTCCCGGCAGGGAATGCCACGGAGCT
                                                                                                                                                                                                                                   Conservative
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/gene="B10D6.060"
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/note="weak similarity to N-terminal region of
gene:CG11008, Drosophila melanogaster, TREMBL:AE003540
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/number=1
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                                                                                                                                                                                                                                                   38.9%;
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                                                                                                                                                                                                                             Score 262.4; DB 15;
Pred. No. 1.7e-44;
D; Mismatches 216;
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TRU24191
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Hypocrea jecorina
Hypocrea jecorina;
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Hypocreomycetidae; Hypocreales; Hypocreaceae;
                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (06-APR-1995) Willem
Stellenbosch, Microbiology, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 786)
la Grange, D.C., Pretorius, I.
Expression of a Trichoderma
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Trichoderma reesei beta-xylanase
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                                                      /gene="XYN2"
105. .776
/gene="XYN2"
/note="endo-beta-1,4-xylanase;
/codon_start=1
/product="beta-xylanase precursor"
/protein_id="AAB50278.1"
/db_xref="GI:780816"
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                                                                                                                                                                                                       /mol_type="mRNA"
/strain="QM 6a"
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van Zyl, W.H.
beta-xylanase

gene (XYN2) in

Sordariomycetes; Hypocrea.

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Humicola insolens
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Eukaryota; Fungi; Ascomycota; 1 (bases 1 to 1039)
Dalboege, H. and Hansen, H.P.H.
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204. .773
/gene="XYN2"
/product="beta-xylanase"
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Direct Submission
Submitted (04-NOV-1993) H. Dall
Nordisk A/S, Symbion, Fruebjer
Location/Qualifiers
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2 (bases 1 to 1
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                                                                                                                                                                                                                                                                                                       CATCGTCGAGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGT 416
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/product="endo-1,4-beta-xylanase"
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/db_xref="GOA:P55334"
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PSIDGTRTFQQYWSIRKNKRVGGSVNMQNHFNAWQQHGMPLGQHYYQVVATEGYQSSG
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/mol_type="mRNA"
/db_xref="taxon:34413"
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Pred. No. 8.4e-40;
); Mismatches 209;
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Indels Length

6; Gaps

1039;

ACGCACCTAGCAT 476

ACAAGGGCACATT 474

TCGTCGAGTACTA 414

TGAATGTCAACGG AGCGTGTCGGAGG

596

594 536 534

GCGCACCAGCGG

GCTACTTCAACCC 354 GTGTTTACCAGCC 296 ACTICGICGGIGG

297

ACCTCGTCGGTGG 236

AGGTTCAGTACAC

237

CCAACGCCGAGGG

177

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Sequence
165436
165436.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 1123)
Berka, R.Michael., Yoder, W., Takagi, Aspergillus expression system
Patent: US 5667990-A 3 16-SEP-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown
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                                                      TACCGTCCAGACGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGG
                                                                                                     CGACGGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGG
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/mol_type="unassigned
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); Mismatches 210;
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Aspergillus
BD006885
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Berka, R.M., Yoder, W., Takagi, S. and Boomi
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JP 2001025393-A/2.
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Humicola insolens
                         CATCGTCGAGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCG
                                                                                                                                         AAAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCC 296
                                                                                                                                                                                          CAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAA
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                                                                                 AAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCGCTGGTCGAGTATTA 356
                                                                                                                                                                       CAACCTCGAGGGCAGCCGCTACCAGGTCAGATGGCGTAACACCGGCA
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JP 2001025393-A/2
30-JAN-2001
17-MAY-2000 JP 2000185449
01-DEC-1993 US 08/161675
RANDY M BERKA, WENDY YODER, SHINOBU TAKAGI,
CARAPPAN CHETYER BOOMINAZAN
C12N15/09, C12N1/15, C12P21/02//(C12N15/09, C12R1:685),
(C12N15/09, C12R1:69), (C12N1/15, C12R1:66), (C12P2C12N15/00)
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nilarity 64.4%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers (126). (806).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Humicola insolens"
/mol_type="genomic DNA"
/db_xref="taxon:34413"
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                                                                                                                                                                                                                                                                                                                                              Score 239; DB 6; Pred. No. 1.8e-39; Mismatches 210;
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system.
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                           ATCTAGGAACTGT 416
                                                                                                                                                                                                                                                                                     CCAACGGCGAGGG 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R1:66), (C12N15/09,
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CAAGGCACATT 553
                                                                                                              CTACTTCAACCC 433
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                                                       CGTCGAGTACTA 493
                                                                                                                                                                                       CCTCGTCGGTGG 236
                                                                                                                                                                                                                               GGTTCAGTACAC 316
                                                                                                                                                                                                                                              GGCCACGTACAC 176
                                                                                                                                                                       CTTCGTCGGTGG 376
                                                                                                                                                                                                                                                                                                              CAACTCGGAGGG 116
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Unpublished
2 (bases 1 to 841)
Min,S.Y., Kim,B.G. a
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Trichoderma |
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AY156910.1 (
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Direct Submission

Submitted (30-SEP-2002) Forest and Environmental Science, Konk Submitted (30-SEP-2002) Forest Andrew Submitted (30-SEP-2002) Forest Andrew Submitted (30-SEP-2002) For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 841)
Min, S.Y., Kim, B.G. and Ahn, J.-H.
Purification, Characterization,
Trichoderma Strain SY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trichoderma sp. SY
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trichoderma.
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                       CGAAAAGCGACAGACACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTG
                                                                               CCTCGCCGGCTTTGCCGGTGTTGCCGGAGTCCTGTCGGCTCCTACTGAAGACGTGCAAGT
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                                                                                                                    CCTTGCGGCCTTAGCCGCGACTGGGGCCCTGGCCTTCCCGGCAGGGAATGCCACGGAGCT
 CGANANGCGTCAGGTCATTGGCCCCGGCACTGGCTTCAACAACGGCTACTACTACTCGTA
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                        /codon_start=1
/product="xylanase"
/product="xylanase"
/protein_id="AAN78423.1"
/protein_id="AAN78423.1"
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/SYWNDGHAGVTYTNGAGGSFSVNWANSGNFVGGKGWNPGSSTRTINFSGSYSPNDNS
YLSVYGWSKNPLIEYYIVENFGTYNPSTGATKLGEVTLDGSVYDIYRTQRVNQPSIIG
TATFYQYWSVRRSHRSSGSVNVGNHFNAWRNLGLTLGQLDYQIIAVEGYFSSGSANIN
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/db_xref="taxon:215577"
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                                                                                                                                                           Score 230.8; DB 15;
Pred. No. 9.3e-38;
D; Mismatches 252;
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Trichoderma viride scomplete cds.
AY320048
AY320048.1 GI:32481
                                                                                                                                                                                                                                                                                                                                                                             Yang, Z.W.
                                                                                                                                                                                                                                                                                                                  Cloning and characterization Trichoderma viride YNUCC0183 Unpublished
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1 (bases 1 to 672)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trichoderma
                                                                                                                                                           Submitted (10-JUN-2003) Key Laborer Fermentation Technology of Yunna University, 2 North Road, Green Location/Qualifiers
                                                                                                                                                                                                                                                                                  Li,W.P.,
                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                            Yang, Z.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trichoderma viride
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                           Zhang, Q.,
                                                          /mol_type="mRNA"
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/db_xref="taxon:5547"
codon_start=
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                                                                                                                                                                                                                                                                                     Liu, W.J. and
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ACCESSION
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DEFINITION
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al Similarity 60.6%;
393; Conservative
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Fusarium oxysporum f
gene, complete cds.
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           Fusarium oxysporum f. sp. lycopersici
Fusarium oxysporum f. sp. lycopersici
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusari
Fusarium oxysporum complex.
                                                                                                              AF246830.1
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IIGTATFYQYWSVRRNHRSSGSVTVANHFNAWRNLGLTLGTLDYQIIAVEGYFSSGNA
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Pred. No. 3.3e-37;
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Molecular characterization of a novel endo-beta-1 from the vascular wilt fungus Fusarium oxysporum Curr. Genet. 40 (4), 268-275 (2001)
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Hera,C., Gomez-Gomez
Direct Submission
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Submitted (17-MAR-2000)
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TGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAG
                                                                                                                                                 GAGACCACTCGCACCAACGCCCCTTCAATCGACGGTACTCAGACCTT
                                                                                                                                                                                      AAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCTT
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                                                                                                     TCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGCTGCCACTTCGACGCC 567
                                                                                                                                                                                                                                  TCCAGCGGTGCTACCAAGAAGGGCACCGTTGAGGCCGATGGCAGCAC
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llarity 64.7%;
Conservative
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DGTQTFQQYWSVRQQHRSTGSVDTGLHFDAWEKAGMKLGTHDY)
MTVSEGASSGGGAGGSTGGDASQGGDSQQGGDVQQGGDASQGGI
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<686. .>1667
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Trichoderma viride
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/db_xref="UniProt/TrEMBL:Q9UVF9"
/translation="MVSFTTLLAGFVAVTGVLSAPTETVEVVDVEKRQTIGPGTGFNN
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GNSYLSVYGWSKNPLIBYYIVENFGTYNPSTGTTKLGEVTSDGSVYDIYRTQRVNQPS
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/produCt="endo-1,4-beta-xylanase"
/protein_id="CAB60757.1"
/db_xref="GI:6434133"
/db_xref="GOA:Q9UVF9"
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/mol_type="mRNA"
/db_xref="taxon:5547"
<a href="faxon">faxon</a>
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/EC_number="3.2.1.8"
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Oryza sativa (japonica cultivar-group)
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Spermatophyta; Magnoliophyta; Liliopsida;
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ta; Tracheophyta; Poaceae;

Kagawa, I.,

PLN 24-JUL-2003:002-168-G08, full

727 662 ACTACTACCAGAT

614

FCACGGTTGCGAA 621

SAACGGCCACCTT

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JOURNAL
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 365; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bource
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FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
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and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
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Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katch, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, A., Murata, M.,
Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A., and Hayashizaki, Y.
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Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Submitted (27-AUG-2002) Head (27-AUG-2002) Fene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, 305-8602, Japan (E-mail:skikuchi, 2007)
Tel:81-29-838-7007, Fax:81-29-838-7007)
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Yoshimura, A.
GTGCAGTGGCGCAACACTGGCAACTTCGTCGGTGGGAAGGGATGGAACCCCAGG---AACC
                                   ATCAGCTGGGGAAGATGGCCGGTAACCTCGTCGGTGGAAAGGGGCTGGAACCCCCGGCCTGAAC
                                                                                                                 TĠĠŦĠĠĂĊĊĠĂŦĠĠĊĠĠĊĠĠĊŦĊŦĠĊĊĂŦĂŤĂĊĂĊĊĂŦĠĠĠĊĠĠĠĠĠĊŦĊĊĀĄĠŦĀĊĄĊŦ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       31.6%;
                                                                                                                                                                                                                                                                                                                                                 Score 213; DB 15;
Pred. No. 4.6e-34;
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IFR 85 - ESBS -UIP, Boulevard Sebastien Brant - BI
Illkirch-Graffenstaden, Alsace 67412, France
Location/Qualifiers
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Hatsch,D., Phalip,V. and Jeltsch,J.-M.
The xylanases of Gibberella zeae
Unpublished
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Bukaryota; Fungi; Ascomycota; Pezizomycotina;
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                                                                                                                                                                                                                                                                                                                                                                                 organism="Gibberella/mol_type="mRNA"
                                                                                                                                                                                                                                                                                   'gene="xyl19"
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AAD17927

AAQ74098

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AAZ28864

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ADL23221

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Biocceleration Ltd.
Aat40742 Xylanase
Aat43010 Endo-1,4-
Aas13813 DNA encod
Aad17927 Thermomyc
Aag74098 Humicola
Aag94952 Humicola
Abg80362 A. fumiga
Abg80364 A. fumiga
Aaz28865 Streptomy
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Adx70798 Streptomy
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Adj35015 DNA encod
Aat63044 Aspergill
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Aat64930 Actinomad
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| Adj35017 | ADJ35017 | 12 | 1071 | _ | 150.6 | 44 |
| Adj34999 | ADJ34999 | 12 | 1065 | - | 150.8 | 4 ω |
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| Adj35037 | ADJ35037 | 12 | 1047 | 23.1 | 156.2 | 41 |
| Aaq69150 | AAQ69150 | N | 1581 | 23.6 | 159 | 40 |
| Adj35001 | ADJ35001 | 12 | 1083 | 23.7 | 159.8 | 39 |
| Adj34967 | ADJ34967 | 12 | 1083 | 23.8 | 160.8 | 38 |
| Ad | ADJ34979 | 12 | 1044 | 23.8 | 160.8 | 37 |
| Aaq28828 | AAQ28828 | N | 516 | 24.3 | 164 | 36 |
| Aaq74638 | AAQ74638 | N | 927 | 24.4 | 164.6 | 3 5 |
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| Abq80366 | ABQ80366 | 10 | 942 | 24.5 | 165.4 | ω W |
| Adj35005 | ADJ35005 | 12 | 1044 | 24.5 | 165.6 | 32 |
| Adj34953 | ADJ34953 | 12 | 1041 | 24.6 | 165.8 | 31 |
| Aaq36563 | AAQ36563 | N | 675 | 24.9 | 168.4 | 30 |
| Adj35039 | ADJ35039 | 12 | 1137 | 25.2 | 170 | 29 |
| Adj34983 | ADJ34983 | 12 | 1074 | 25.2 | 170 | 28 |
| Aaq43458 | AAQ43458 | 2 | 572 | 25.5 | 171.8 | 27 |
| Abq80361 | ABQ80361 | 10 | 712 | 26.8 | 181.2 | 26 |
| Aat71585 | AAT71585 | N | 1281 | 26.9 | 181.8 | 2 5 |
| Aaq03405 | AAQ03405 | N | 1057 | 27.2 | 183.4 | 24 |
| Adj34949 | ADJ34949 | 12 | 1047 | 27.4 | 185 | 23 |
| Adj35009 | ADJ35009 | 12 | 1059 | | • | 22 |
| Aaq90388 | AAQ90388 | N | 1273 | 27.8 | 187.8 | 21 |
| Abq80363 | ABQ80363 | 10 | 739 | 28.0 | 189.2 | 20 |

RESULT 1 AAT40742 ID AAT40742; XX AC AAT40742; AC AAT4074 Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermoascus; Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia; Byssochlamus; Paecilomyces; animal feed additive; in-vivo breakdown; plant cell wall; growth rate; feed conversion; ss. Location/Qualifiers 31. .708

ALIGNMENTS

/*tag= a /product= "xylanase"

Page 45-46; 69pp; English.

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Matches 675
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Similarity 100.0%;
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                                                                                                                                                                                                                                                The sequence encodes an endo-1,4-beta-D-xylanase from Thermomyces lanuginosus (Humicola lanuginosa), which may be used as a breadimproving additive. The enzyme may be expressed recombinantly from a plasmid pYES2.0 vector in Saccharomyces cerevisiae DSM 10133 (claimed), and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour, optionally along with other enzymes (amylase, maltogenase, lipase, cellulase, hemicellulase, pentosanase, glucose- oxidase, laccase, protease and/or peroxidase). The enzyme combines particularly well with amylolytic enzymes, and may be used to improve baking properties of flour and/or dough, by increasing volume and improving texture, flavour, crumb softness, freshness and anti-staling properties, while improving dough machinability and stability. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endo-1,4-beta-D-xylanase; xy
Humicola lanuginosa; bread;
flour; baking; dough; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bread improving additive alpha-amylase, increases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermomyces lanuginosus; (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endo-1,4-beta-D-xylanase
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jorgensen
                                                                                                                                                                                                                              Sequence
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DB; AAW05187.
              181
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                                                                                                                                                                                          Similarity
                                                                                              CCGGCAGGGAATGCCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGG 120
                                                                                                                                             ATGGTCGGCTTTACCCCCGTTGCCCCTTGCGGCCTTAGCCGCGACTGG
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                                                   CACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAAC 180
             CTGGAAGGCGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCT
                                  CACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGC
                                                                                                                                  ATGGTCGGCTTTACCCCCGTTGCCCCTTGCGGCCTTAGCCGCGACTGG
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/product= "Endo-1,4-beta-D-xylanase"
/note= "EC-3.2.1.8"
709. .983
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d; enzyme;
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                                                                                                                                                                             Score 675; DB 2;
Pred. No. 2.6e-174;
); Mismatches 0;
                                                                                                                                                                                                                              277
                                                                                                                                                                                                                                                                                                                                                                                                                                              xylanase from Thermomyces - and opt., improves anti-staling properties etc.
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CGTCGGTGGAAAG
                                       CACGTACACCAAC
                                                                                                                                  GCCCTGGCCTTC
                                                                                                                                                           GGCCCTGGCCTTC
                                                                                                                                                                                                        983;
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 The invention relates to a variant fragment having xylanase activity,
                                          Disclosure; Page 64; 70pp;
                                                                    Novel variant xylanase polypeptide or its fragment useful for degrading or modifying plant cell wall, comprises amino acid modifications such that the polypeptide has altered sensitivity to xylanase inhibitor.
                                                                                                                              WPI, 2001-596834/67.
                                                                                                                                                                                                              08-MAR-2000;
27-JUN-2000;
                                                                                                                                                                                                                                                        08-MAR-2001;
                                                                                                                                                                                                                                                                                                                                        Thermomyces lanuginosus.
                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding
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                                                                                                                                                                                                                                                                                                             WO200166711-A1
                                                                                                                                                                                                                                                                                                                                                                                   Xylanaве А;
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                                                                                                                                                                                     (DANI-) DANISCO
                                                                                                                                                                                                                                                                                                                                                                  nase A; plant cell wall; baking; cereal; starch production; wood; pulp bleaching; hemicellulose; arabinoxylan; foodstuff; bread; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       691
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                                                                                                                                                                                                              2000GB-00005585.
2000GB-00015751.
                                                                                                                                                                                                                                                                                                                                                                                                            Thermomyces lanuginosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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xylanase polypeptide (; comprising one or more
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TTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGC
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100.0%; Pred. No. 6.1e-149;
Live 0; Mismatches 0;
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RESULT 4
AAD17927
ID AAD1
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AC AAD1
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DT 10-E
XX
DE Ther
XX
XX
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XY
AX
XX
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                                                                    AAD17927;
                             Thermomyces lanuginosus codon optimised xylanase gene
                                                                                      standard; DNA; 678
                                                (first
                                                entry)
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Xylanase;

Pichia

cell; heterologous

nucleotide;

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timisation;

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Best Local S
Matches 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heterologous nucleotide sequence encoding a polypeptide of interest, where the codon usage of the sequence has been adjusted to match the preferred codon usage of P. methanolica. The invention also relates to a method for producing high yields of heterologous codon optimised polypeptide in a Pichia cell. The Pichia cell is useful for producing a polypeptide of interest, where the polypeptide is encoded by a nucleotide sequence heterologous to P. methanolica. The present sequence is Thermomyces lanuginosus codon optimised xylanase gene which is the heterologous DNA used in the invention
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15-MAR-2000;
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                                                                  GTCGAGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAG
                                                                                                                         GGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCGCTGGTCGAGTATTACATC
                                                                                                                                                                           GGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAAC
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Pred. No. 2.2e-91;
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Query Match Best Local S Matches 391

Local Similarity

35.4%; ilarity 64.4%; Conservative

Score 239; DB Pred. No. 4.7e 0; Mismatches

e 239; DB 2; I . No. 4.7e-55; ismatches 210;

Length

1123;

Indels

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391;

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RESULT 5
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XX AAQ7
XX YX Humi
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XX W095
PN W0
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25-MAR-2003
14-NOV-1995
                                A DNA fragment (AAQ74098) encoding H. insolens xylanase isolated from pYES (DSM 6995) and inserted into pHD414 (promoter and AMG terminator) to form pAXX40-1-1-1. This pJaL77 (imparting hygromycin B resistance) were used to t protoplasts of A. foetidus NO953. The xylanase yield was (Updated on 25-MAR-2003 to correct PN field.) (Updated or correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1993;
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Sequence
                                                                                                                                                                                                                      Disclosure; Page 35-36; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-215270/28.
P-PSDB; AAR75421.
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                                                                                                                                                                                                                                                                                      Aspergillus foetidus cells
fungal lipase or xylanase,
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RESULT 6
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AC AAQ9
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DT 25-M
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XX YJ1a
XX YJ1a
XX Hum1
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02-DEC-1995
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Matches 391
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 ABQ80362;
                                            ABQ80362
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or mycotoxin.
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fungal enzyme, provide high yields without significant prodn. of protease
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P-PSDB; AAR78231.
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                                                                                                                                                                                                                                                                                                                                           TACCGTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGG 596
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Conservative
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Pred. No. 4.7e-55;
0; Mismatches 210;
                                            ВP
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ACGCACCTAGCAT 476 ACAAGGGCACATT 553

GCGTGTCGGAGG

673 536

GCGCACCAGCGG

CGAGTCCGACAT

790

GCCGCT---CGG

730

TCGTCGAGTACTA

ATCTAGGAACTGT

416 493 GCTACTTCAACCC

433

STGTTTACCAGCC

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Cenzyme such as tannase, cellulase, plucose oxidase, glucoamylase, ce phytase, beta-galactosidases, invertase, lipase, alpha-amylase, laccase, compositions comprising the tannase are cuseful for modulating the amount of compositions comprising cellulase are cuseful for modulating the amount of compositions comprising cellulase are compositions comprising cellulase are compositions comprising cellulase are compositions compositions comprising cellulase are compositions comprising cellulase are useful for modulating the amount of composition. Compositions comprising phytase are useful for modulating the amount of myo-inosition comprising cellulase are useful for modulating the amount of laccose in a composition. Compositions comprising sucrase or invertase are useful for modulating the amount of compositions comprising lipase are useful for composition in a composition composition compositions comprising alpha-amylases are useful for modulating the amount of composition. Compositions comprising lipase are useful for composition composition compositions comprising lipase are useful for modulating the amount of compositions comprising comprising comprising the amount of composition compositions comprising composition compositions comprising composition compositions compositio
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P-PSDB; ABB80185.
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the making of food and
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RESULT 8
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ID ABQ8
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Best Local S
Matches 413
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                                                                                                                  ABQ80364
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                                                                                                                                                                                                                                                                                                                                    <u> ACCGTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTT</u>
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                                                                                                                   standard; cDNA;
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No. 3.5e-51;
Thes 249;
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Gene; enzyme;

tannase; cellulase;

glucose

oxidase;

gluce

amylase; phytase;

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polygalacturonase; xylanase; gallate ester linkage; detergen glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; glyceride; starch; maltodextrin; oxidated phenolic compound; polygalacturonic acid chain; xylan; xylo-oligomer; food; fee
                                                                                                                                                                          beta-galactosidase; invertase; lipase; alpha-amylase;
tea liquor; cleaning ability; ss.
                                                                                                    e; detergent; cellu
tea leaf; sucrose;
                                                                                                                                                                          laccase;
                                     feed; beverage;
                                                                                                                                            cellulose;
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Aspergillus fumigatus.

Location/Qualifiers product= "Xylanase

WO2003012071-A2

2002WO-US024842

03-AUG-2001; 2001US-0309870P

ELITRA PHARM INC

Storms R, Roemer T, Bussey

WPI; 2003-332729/31. P-PSDB; ABB80186.

Novel isolated Aspergillus fumigatus industries such as those involved in beverages, textiles and detergents. polypeptide, useful in the making of food and various feed,

Claim 2; 165-66; 169pp; English

The sequences given in ABQ80319-66 encode enzymatic proteins derived from CC A. funigatus. The resulting proteins display the catalytic activity of an CC enzyme such as tannase, cellulase, glucose oxidase, glucosenylase, phytase, beta-galactocosidases, invortase, lipase, alpha-amylase laccase, collygalacturonase or xylanase. Compositions comprising the tannase are useful for modulating the amount of cellulase in a composition. Compositions comprising cellulase are useful for modulating the amount of cellulase in a composition. Composition comprising phytase are useful for modulating the amount of cellulase in a composition. Composition comprising comprising phytase are useful for modulating the amount of a composition. Compositions comprising comprising the amount of plucose oxidase are useful for modulating the amount of phytase are useful for modulating the amount of myo-inositol phosphates or modulating the amount of glyceride in a composition. Compositions comprising phytase are useful for modulating the amount of glyceride in a composition composition comprising phytase are useful for modulating the amount of camposition comprising comprising sucrase or maltodestring in a composition composition comprising comprising slipase are useful for modulating the amount of phytase are useful for modulating the amount of oxidated phenolic composition composition. Compositions comprising comprising polygalacturonases are useful for modulating the amount of oxidated phenolic composition composition. Compositions comprising comprising polygalacturonases are useful for modulating the amount of oxidated phenolic composition. Compositions comprising polygalacturonases are useful for modulating the amount of oxidated phenolic composition composition. Compositions comprising comprising polygalacturonases of the accuse of the phytagetus proteins and corresponding DNA s are useful for modulating the amount of xylan or xylo-oligomers to identify duplicated genes of paralogs having the amount of paralogs and making of food capt

Location/Qualifiers

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RESULT 9
AAZ28864
ID AAZ2
XX
AC AAZ2
XX
DT 27-A
DT 01-F
XX
DE Stre
XX
XW Xyla
KW Xyla
KW pulp
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OS Stre
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Best Local Similarity
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                                                       Xylanase; plasmid;
pulp-bleaching; ds
                                                                                                                              27-AUG-2003
01-FEB-2000
                             Streptomyces
                                                                                                 Streptomyces
                                                                                                                                                                      AAZ28864;
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                                                                                                                                                                                                 AAZ28864 standard;
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                                                                                                  olivaceoviridis xylanase
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                                                                     expression;
                                                                                                                                                                                                 DNA; 1195
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                                                                      E.coli; xylo-oligosacchar
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No. 2.4e-50;
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ACCAACCCCTTGA 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A xylanase gene, pulp-bleaching.
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P-PSDB; AAY44183.
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SEIBUTSUKEI TOK
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                                        TACAACGCCCCCTCCGTGGAAGGCACCAAGACCTTCAACCAGTACTGGAGCGTCCGGCAG
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                                                          ACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGC
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418. .990
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RESULT 10
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pulp-bleaching; ds
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RESULT 11
ADK70798
ID ADK70
XX ADK70
AC ADK70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces animal feed;
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 Heat-resisting, antiproteinase acidic-neutral xylanase
                                           WPI; 2003-514374/49.
P-PSDB; ADK70799.
                                                                                                                                                                                                                                       14-SEP-2001;
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RESULT 12
ADL23221
ID ADL23
XX
AC ADL23
XX
DT 20-MA
XX
DE A. ni
XX
KW 88; g
KW biscu
KW crumt
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CS Asper
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FH Key
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Best Local Similarity
Matches 353; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes the Streptomyces olivaceoving enzyme. The xylan enzyme has good heat stability, high acacidic and neutral pH. The xylan enzyme can be used as a and can be widely used in animal feed.
                                                                   ss; gene; A. niger; (hemi)obiscuit; elasticity; stabicurumb structure; softness;
                                                                                                                         A. niger (hemi)cellulase NBE021 coding sequence
                                                                                                                                                      20-MAY-2004
                                          Aspergillus
                                                                                                                                                                                 ADL23221;
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                                                                    ; A. niger; (hemi)cellulase; filamentous fungus; elasticity; stability; stickiness; extensibility ructure; softness; flavour.
                                                                                                                                                                                                                                                                                                                                                                                                               GACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCCACTTCGACGCC
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                                          niger
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larity 62.7%;
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ismatches 201;
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activity under
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y; machinability;
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                                                                                                                                                                                                                                                                                                                                               This sequence encodes an A. niger (hemi)cellulase NBE021. The (hemi)cellulase coding sequences of the invention are derived from a filamentous fungus, preferably Aspergillus niger. The (hemi)cellulase is useful in producing dough, which is useful for preparing a baked product such as bread, biscuits from the dough. Fragments of the (hemi)cellulase is the useful as probes and primers for detecting the expression of (hemi)cellulose mRNA in a biological sample such as a tissue. They are calated sequences. Anti-(hemi)cellulase antibodies are useful for qualitative or quantitative determination of a polypeptide in a biological sample. These antibodies are useful in diagnosing organism is infected with Aspergillus. The dough prepared by using the inventive (hemi)cellulase has increased strength, elasticity, stability, reduced stickiness, improved extensibility and machinability. The grepared baked product has improved crumb structure, softness and flavour. The (hemi)cellulase has higher specificity towards the substrate, is less antigenic and produces less undesirable side
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Best Local S
Matches 398
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AAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCA
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 The invention describes an isolated or recombinant polyhaving 50% or more identity to 190 300-1200 residue ami (S1), given in the specification, over a region of 100 and the polypeptide as thermostable xylanase activity.
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                                                                                                                                                           Novel xylanase recombinant polypeptide useful for improv texture, treating paper, eliminating microorganisms.
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Best Local (
Matches 37(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dough conditioning; beverage production; as a nutritional supplement in animal feed; reducing lignin in a wood or a wood product; and for eliminating and protecting animals from a microorganism comprising xylathe polynucleotide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylanase activity which involves amplification of a template nucleic acid with a primer pair capable of amplifying (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis. This sequence encodes xylanase protein isolated from an environmental
               Aspergillus
                                              17-OCT-2003
22-JUL-1997
                                                                                                                           AAT63044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCGCGCTGGCGCGCTCGCCGCCGCTGATGCTGCCGGGCACCCCAGGCCGACACGGTC
                                                                                                                            etandard;
                                                                                                                                                                                                                                                                                                                                                     CAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACT
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                                                                                                                                                                                                                                    AGCAGCGGCTATGCTCGCATCACCGTTG
                                                                                                                                                                                                                                                                 GCCGGGATGCCGCTCGGCAACTTCAGCTACTACATGATCATGGCCACCGAGGGCTACCAG
                                                                                                                                                                                                                                                                                        GCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTC
                                                                                                                                                                                                                                                                                                                              CAGGCGAAGCGGACCGGCACCATCACGACCGGCAACCACTTCGACGCGTGGGCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACTCGGGCAGCTTCAACCCCTCCGGCAACGCGTACCTGGCGCTCTACGGATGGACGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCACGACCAACCAGGAGGGCACCAACAACGGCTACTACTACTCGTTCTGGACCGACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1008
                                                                                                                                                                                                       AGCAGCGGCAGCTCCAGCATCAACGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                          ----AGTACAAGGGCACCGTCACCAGCGACGGCGCACCTACGACATCTACAAGACGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCGGCAACTTCGTCGCGGGCAAGGGCTGGGCCAACGGCGGCCGGA---CCGTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGGCACCGTCTCCATGAACATGGGCTCCGGCGGTCAGTACAGCACCTCGTGGCGCAAC
                 niger
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                                              (revised)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 192 A; 362
                 xylanase
                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGAGTACTACATCGTCGACAACTGGGGCACCTACCGGCCCACGGGCG--
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59.9%;
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Pred. No. 9.9e-45;
0; Mismatches 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; 331 G;
                                                                                                                                                                                                       691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 29.4
Best Local Similarity 61.9
Matches 354; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A cDNA clone (AAT63044), deposited as CBS 590.95, codes for a xylanase (AAW14597) of Aspergillus niger N400 (CBS120.49). It was isolated using a method for identifying a DNA fragment encoding a protein of interest. The method involves the direct screening of a cDNA library prepd. in bacteria (e.g. E. coli) transformed with DNA from a eukaryotic organism (e.g. A. niger) that produces the protein. Screening for xylanase-producing clones can be performed on agar plates containing oat spelt xylan and RBB-xylan. The method was utilised in the identification of cDNA clones (AAT63042-46) coding for A. niger cellulase, xylanase and arabinoxylan degrading enzymes (AAW14595-99). (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying DNA fragments encoding proteins, e.g. discovery - by direct screening of a cDNA library with DNA from eukaryotic organism producing the p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endoxylanase; xylanibrary screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-OCT-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9713853-A2
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DB; AAW14597.
                                                                                                                                      338
                                                                                                                                                                                                                                                                                                                                                   142
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                                                                                                                                                                                                                                                                                                          GAGCGCAGGCCACCTACCCAACCTGGAAGGCGCGCACCTACGAGATC
                                                                                                                                                                                                                                                                                                                                                                 CAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     851 BP; 201 A;
 GCGTCAACGCACCTAGCATCGACGGCACCCAAACCTTCGACCAATACT
                                              GCÁCGTÁCAAGGGCÁCCGTCACCTCGGÁCGGATCCGTTTÁCGATATC
                                                                       CTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTC 457
                                                                                                      ACCCTCTGATCGAGTACTACATCGTCGAGTCCTACGGCGACTACAACC
                                                                                                                                    ACCCGCTGGTCGAGTATTACATCGTCGAGAACTTTGGCACCTATGATC
                                                                                                                                                                 ACAGCGGCACCTTCACCCCTAGCGGCAACGGCTACCTCTCCGTCTAT
                                                                                                                                                                                                                                                         GCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACT 277
                                                                                                                                                                                                                                                                                       GTGGAGACGTGACCTACACCAACGGAGATGCTGGTGCCTACACTGTTGAGTGGTCCAACG
                                                                                                                                                                                                                                                                                                                                                 CGACCCCGAGCTCGACCGGCGAGAACAACGGCTTCTACTACTTCTTGGACCGACGGCG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 19-20;
                                                                                                                                                                                                                             TGGGCAACTTTGTCGGTGGAAAGGGCTGGAACCCCGG---AAGTGCGC
                                                                                                                                                                                              TTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                niger; strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xylanase;
ning; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HC,
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                                                                                                                                                                                                                                                                                                                                                                                                                         29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 C; 224 G; 182 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 198.4; DB 2;
Pred. No. 5.5e-44;
); Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Visser
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ry in bacteria transformed
protein.
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GGTCGGTCCGCC
                                              PACACGGCTACCC 498
                                                                                                                                                                                                                                                                                                                   AGCTGGGGAGATG
                                                                                                         CCGGCAGTGGAG 438
                                                                                                                                                                                                                             AGGACATCACCT 318
                                                                                                                                                                                                                                                                                                                                                                              GGAGTGACGGTG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                        851;
                                                                                                                                    CTTCCTCCGGTG 397
                                                                                                                                                                 GCTGGACCACTG 378
                                                                                                                                                                                               GTTGGACCCGCA 337
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ص
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217

261

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RESULT 15
AAX90405
ID AAX90
XX AAX90
XX 16-OC
DT 25-MA
DT 28-SE
XX ACTIN
KW CHERT
KW PAPER
XX PT CDS
FT CDS
FT CDS
FT CDS
FT CDS
FT ACTIN
XX WPI;
DR WPI;
DR WPI;
DR WPI;
DR P-PSI
XX PACTIN
XX WPI;
DR P-PSI
XX ACTIN
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The present invention describes a culture medium obtained from the culture of a recombinant host cell that is not Actinomadura flexuosa and that been transformed with a vector encoding a protein having xylanase activity, where the protein comprises an amino acid sequence from a cylanolytic fragment of the amino acid sequence in AAY24480 or AAY24481.

Also described is an enzyme preparation derived from the culture medium.

Condifying plant biomass properties, especially the reduction of lignin content in pulp and paper processing. The xylanases are hemicellulases which partially degrade the hemicellulose and enhance the extractability of lignins by conventional chemical bleaching of wood pulp. It can be used alone or as a supplement to other treatments that reduce lignin content of wood pulp, increase its drainability or decrease its water retention. The culture medium can be used directly without the need to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2003
25-MAR-2003
28-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX90405
                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fagerstrom R, Maentylae A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomadura xylan sequences and method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1994;
31-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomadura
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)B; AAY24480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROEHM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGGAATGAA----CCTGGGTACTCACAACTACCAGATCGTGGCTACCGAGGGTTACCAGA
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ALIGNMENTS

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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordar
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordar
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibbere
1 (bases 1 to 860)
Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Z
Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Pl
Kendra,D.F., Town,C.D. and Whitelaw,C.A.
Analysis of 87,000 expressed sequence tags reveals a
spliced introns in multiple genes of the fumonisin g
Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR
                                                                                                                                                                                                                                                                                                                                                                     USDA
1815 N. University St, Peoria, IL
1815 N. University St, Peoria, IL
Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FVMB275TH
Seq primer: AAT TAA CCC TCA CTA AJ
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DR637934
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EST1028559
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/tissue_type="mycelia"
/clone_lib="FvM"
/clone_lib="FvM"
/note="Vector: pBlueScript II SK(+) XR; Site_l
Site_2: XhoI; anamorph: Fusarium verticillioId
FvM was prepared from pooled RNA obtained from
and a 72 hour, liquid GYAM culture from strain
Cultures were vacuum filtered and the mycelial
frozen in liquid nitrogen, ground to a powder,
added to TRIzol Reagent (Invitrogen, Carlsbad
approximately 1 g mycelia per 10 ml TRIzol. Th
                                                                                                                                                                                                                    /organism="Gibberella mon
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVMB275"
                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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ticillioIdes. Library
ained from a 48-hour
rom strain M-3125.
e mycelial mats were
a powder, and then
Carlsbad (A) at
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      The cDNA was
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VERSION
KEYWORDS
SOURCE
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       JOURNAL COMMENT
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AUTHORS
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Local Similarity
hes 442; Conserv
sequence.

N DR643290

DR643290.1 GI:70718124

EST.

Gibberella moniliformis

SM Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

E 1 (bases 1 to 883)

E 1 (bases 1 to 883)

S Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L, Lee, Y.

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

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Unpublished (2005)

Contact: Brown, D.W.
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USDA
1815 N. University St, Peoria,
Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FVMCX47TH
Seq primer: AAT TAA CCC TCA CTA
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                               CTTCGACGCCTGGGAGAAGGCTGGTATGAAGCT--
                                                     CTTCGACGCCTGGGCTCGCGCTTTGAATGTCAACGGTGACCACT
                                                                                                             GCAGTACTGGTCTGTTCGCCAGCAGCATCGCTCTACTGGTAGCGTTG
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Pred. No. 1.1e-69;
); Mismatches 208;
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AGACGGGCTGCCA 557

ACACTGGTCTTCA

578

ACTACCAGATCCT ACTACCAGATCGT 617

635

ACGGTAGCATCTA 437

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CCCAAACCTTCGA

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618 600

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Best Local Similarity
Matches 411; Conser
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49478 5', mRNA sequence.
DR037502
DR037502.1 GI:66839397
EST.
Solanum tuberosum (potato)
                                                                               181
                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                           411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 882)
Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., Do Koeyer,D., Audy,P., Goyer,C., Li,X.-Q., Wang-Pruski,G. and Rogeneration of ESTs from late blight-challenged potato tubers Unpublished (2005)
Contact: Barry Flinn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                    CACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGG
                              AAGGCCGGTGGAGGTACTCCCTGACCTGGAGCGGCAACGGCAACGTCGTTGCTGGAAAG
                                                                               CTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAG 240
                                                                                                                                                                                                                                         CCCGAGACCAGCCCTAACCCCCGCCACA-----AGAAGCGCACGAACCAGACTGGCCAG
                                                                                                                                                                                                                                                                                       ATGGTTTCCCTTACCTACCTTCTCATTGCTGCGTCTGCCGTTGCTGGCGTCTTCGCTGAA
                                                                                                                                                                                                                                                                                                                                                                               ATGGTCGGCTTTACCCCCGTTGCCCTTGCGGCCTTAGCCGGCGACTGGGGCCCTGGCCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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/clone="49478"
/clone="49478"
/tissue_type="Tubers"
/lab_host="XL10-Gold"
/clone_lib="Late Blight-Challenged Tubers"
/clone_lib="Late Blight-Challenged Tubers"
/clone_lib="Late Blight-Challenged Tubers"
/clone_lib="Yector: pBluescript II SK(+) XR; Site_1: EcoRI;
/note="Vector: pBluescript II SK(+) XR; Site_1: EcoRI;
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mol_type="mRNA"
cultivar="Shepody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.6%;
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Pred. No. 1.6e-55;
); Mismatches 258;
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rs Solanum tuberosum cDNA clone
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, E3B 6Z9, CA
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DN588726.1 GI:61239134
EST
Solanum tuberosum (potato)
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Flinn,B., Rothwell,C., Sardana,R., Griffiths,R.
Koeyer,D., Audy,P., Goyer,C., Li,X.-Q., Wang-Pr
Generation of ESTs from late blight-challenged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Canadian Potato Genome Project 921 College Hill Rd, Fredericton, (Email: bflinn@bioatlantech.nb.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2005)
Contact: Barry Flinn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Solanum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCCGCTGGTCGAGTATTACATC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                             primer: T3.
/db_xref="taxon:4113"
/clone="49478"
/clone="49478"
/tissue_type="Tubers"
/lab_host="XL10-Gold"
/clone_lib="Late_Blight-Challenged_Tubers"
/clone_lib="Late_Blight-Challenged_Tubers"
/note="Vector: pBluescript_II_SK(+)_XR; Site_1: EcoRI;
Site_2: XhoI; supplier: Pathogen-challenge_series. Tubers
from_pathogen-free_Solanum_tuberosum_var. Shepody, clone
1756, were inoculated_with_5_ul_of_Phytophthora_infestans
(A2-mating_type), through_2_puncture_wounds_3_cm_apart.
The tubers_were_incubated_1_minute_to_allow_inoculum_absorption. The infection_area_was_outlined_for_future_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tuberosum
                                                                                                                                                                                                                                                                                                          /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
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                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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Seq primer: LT-F1 primer.
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   ACTACCAGATCGTTG-CAACGGAGGGCTACTTCAGCAGCGGCTATGCTC 652
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/db_xref="taxon:51453"
/clone="tric013xe09"
/dev_stage="mycelia"
/clone_lib="T.reesei my.
2003"
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Pred. No. 2.1e-52;
); Mismatches 245;
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culture, Version 6 October

I; Mycelial varying Carbon

Length 744;

Gaps

GCTCCCGCCGCCG 155

AGCGGCTCCGTCA 635

-CGGGACGATGG 692

TCCATCATCGGCA 575

AGCATCGACGGCA 484

GAGGTCACCTCCG

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ATTACCAGATTGTTGCCGTGGGAGGGTTACTTTAGCTCTGGCTCTGCTC 741

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Best Local Similarity 61.6
Matches 400; Conservative
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SM Hypocrea jecorina

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

1 (bases 1 to 799)

S Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,

Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,

Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,

Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.

Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei

J. Biol. Chem. 278 (34), 31988-31997 (2003)
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925 Page Mill Road, 1
Tel: (650) 846-7635
Fax: (650) 621-7817
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                                                                                                                                                          CCGGCGGCAGTTCTCCGTCAACTGGTCCAACTCGGGCAACTTTGTCGGCGGCAAGGGAT
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/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 3 april"
/note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."
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Location/Qualifiers
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/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
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Pred. No. 2.1e-52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA 3
Tel: 706 542 1860
Fax: 706 583 0210
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Sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.
An EST database from Sorghum: oxidatively stressed leaves and roots Unpublished (2003)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales;
clade; Panicoideae; Andropogoneae; Sorghum.
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772 bp mRNA linear 1 OX1_9_D10.g1_A002 Oxidatively-stressed leaves and robicolor cDNA clone OX1_9_D10_A002 5', mRNA sequence. CN133022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer: Sug5 (CTTCTGCTCTAAAAGCTGCG).
Location/Qualifiers
/db_xref="taxon:4558"
/clone="OX1 9 D10 A002"
/lab_host="DH108-T1 phage-resistant E. coli"
/clone lib="Oxidatively-stressed leaves and roots"
/clone lib="Oxidatively-stressed leaves and roots"
/clone lib="Oxidatively-stressed, Vector: pME18S-FL3; Site_1:
/note="Organ: Leaf and Root; Vector: pME18S-FL3; Site_1:
/note="Organ: Leaf and Root; Vector: pME18S-FL3; Site_1:
/note="Oxidatively stressed, Vector: pME18S-FL3; Site_1:
/note="Oxidatively stres
                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Sorghum
/mol_type="mRNA"
/cultivar="BTx623"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dr. Sumio Sugano in Institute of Medical exas A & M University; s and Bioinformatics,
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Poaceae; PACCAD
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VERSION
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AUTHORS
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DR624928
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DEFINITION
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Best Local S
Matches 374
                                    JOURNAL
                                                                                                                                                                                      ORGANISM
                                                                     TITLE
DR624928.1 GI:70699610
EST.
Gibberella moniliformis
Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

E 1 (bases 1 to 639)
S Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Strown, D.W., Cheung, F., Feldblyum, T., Glenn, A.E., Plattner, R.D.,
Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR
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Similarity 63.5%;
74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTGTG, 3-prime DraIII site is CACCATGTGTG). XhoI excises the insert."
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Pred. No. 1.2e-50;
); Mismatches 209;
                                                                                                                                                                                                                                                                                                      639
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1 clone FVIBB05, mRNA
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1815 N. University 9
1815 N. University 9
Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaus
TIGR sequence_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCTAGAACGTGGAAGGCGGCA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCACGGAGCTCGAAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATT 133
                                                                                                                                                                                                                                        CCTATGATCTGTACCAGACCACCCGCTACAACCAGCCCTCTATCGACGGCCAACAGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGCGGTCTACGGTTGGACCCGCAACCCCGCTGGTCGAGTATTACATCGTCGAGAACTTTG
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                                                                         GCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGA 613
                                                                                                                                                                             TCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCT
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TCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTT 663
                                           CTATCTTCAATGCTTGGGCTAATGCTGGCATGAGACT---TGGAAACCACTACTATCAGA
                                                                                                                                           TCAACCAGTACTGGGCCATCCGCCGCAACAAGCGCAGCAGCGGCGCTGTCAACATGCAGA 500
                                                                                                                                                                                                                                                                                     TCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCT
                                                                                                                                                                                                                                                                                                                                                                                      GCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCA 433
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R sequence name: FVIBB05TH
primer: AAT TAA CCC TCA CTA
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                                                                                                                                                                                                                                                                                                                                       CTTACAATCCCGGCTCTGCTGGCCAGCACAAGGGCACCGTCTACAACGACGGCGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 220.4; DB 8;
Pred. No. 4.9e-50;
); Mismatches 211;
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Best Local Similarity
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                                                                                                                                                                                  373;
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Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L, Lee, 1
Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,
Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR
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DR623097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: prowndw@ncaur.usda.gov
TIGR sequence name: FVIAM22TH
Seq primer: AAT TAA CCC TCA CTA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1815 N. University St, Peo
Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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Gibberella moniliformis
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                                                                       ACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCCGCA
                                                                                                                                CCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATT
 CCTACGAGATCAGCTGGGGAGATGGCCGCTAACCTCGTCGGTGGAAAGGGCTGGAACCCCG
                                                                                                            CCTCTGTCCTTGAGGCCCGCCAGGTCACCGGTAACTCTGAGGGTTACCACAACGGATACT
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                                                                                                                                                                                                                                               /clone Tib="FvI"
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioIdes. Library
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10e6 conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIzol. The cDNA was
directionally ligated into the pBlueScript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."
                                                                                                                                                                                  Conservative
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clone_lib="FvI"
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/strain="m3125"
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/clone="FVIAM22"
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63.2%;
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Pred. No. 5e-50;
0; Mismatches 2
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FVIAM22, mRNA
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Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., 2l Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plakendra,D.F., Town,C.D. and Whitelaw,C.A.
Analysis of 87,000 expressed sequence tags reveals alspliced introns in multiple genes of the fumonisin generalished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR
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EST1014866 |
sequence.
DR624738
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TIGR sequence name: FVIB801TH
Seq primer: AAT TAA CCC TCA CTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 309 681 6230 Fax: 309 681 6689 Email: browndw@nca
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Gibberella moniliformis
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EST.
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/tissue type="mycelia"
/clone_Tib="FvI"
/clone_Tib="FvI"
/note="Vector: pBlueScript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI; anamorph: Fusarium verticillioides. Library
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10e6 conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
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                                                                                                                                                                                                                                  /strain="m3125"
/db_xref="taxon:117187"
/clone="FVIB801"
                                                                                                                                                                                                                                                                                                                 /organism="Gibberella
/mol_type="mRNA"
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FVIB801, mRNA
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                                                                                                                                                                                                                                     sequence.
DR631520
Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 719)
Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L, Lee,)
Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
                                                                                                                                                                                                  DR631520.1
EST.
                                                                                                                                                                               Gibberella
                                                                                                                                                                                                                                                                       DR631520
EST1021648
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Similarity 63.2%;
72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTATGATCTGTACCAGACCACCCGCTACAACCAGCCCTCTATCGACGGCCAACAGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTATCGACTCGCCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTACGAGATCAGCTGGGGAAGTGGCGGTAACCTCGTCGGTGGAAAGGGCTTGGAACCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTACTCTTGGTGGTCTGATGGTGGTGGCTATGCCAACTACCGTATGGGTGAGGGAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCTGGAAGGCGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTCTGTCCTTGAGGCCCGCCAGGTCACCGGTAACTCTGAGGGTTACCACCACGGATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACGGAGCTCGAAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #1 filter paper at room temperature under sterile conditions for 4 days. Fungal mycelial was collected, frozen in liquid nitrogen, ground to a powder, and then added to TRIzol Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml TRIzol. The cDNA was directionally ligated into the pBlueScript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)."
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                                                                                                                                                                                   moniliformis
                                                                                                                                                                                                                                                                         Gibberella
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Pred. No. 9.4e-50;
); Mismatches 211;
                                                                                                                                                                                                                                                                                         719
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                                                                                                                                                                                                                                                                                         mRNA
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R.D.,
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Best Local S
Matches 372
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USDA/ARS/NCAUR
USDA
1815 N. University St, Peor
Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
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Seq primer: AAT TAA CCC TCA CTA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTATTCCTGGTGGAGTGACGCTGGAGCCCAGGCCACGTACACCAACCTGGAAGGCGGCA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGCGGTCTACGGTTGGACCCGCAACCCCGCTGGTCGAGTATTACATCGTCGAGAACTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTACGAGATCAGCTGGGGAGATGGCGGGTAACCCTCGTCGGTGGAAAGGGCCTGGAACCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTACTCTTGGTGGTCTGATGGTGGTGGCCTATGCCAACTACCGTATGGGTGAGGGAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACGGAGCTCGAAAAAGCGACAGACAACCCCCCAACTCGGAGGGCTGGCACGATGGTTATT
                                                                                                                                                                                                               CCTATGATCTGTACCAGACCACCCGCTACAACCAGCCCTCTATCGACGGCCAACAGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                             GCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCA 433
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GCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGA 613
                                                                                                                                      TCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCT
                                                                                                                                                                                                                                                                                         TCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCT
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/clone lib="FvI"
/clone lib="FvI"
/clone lib="FvI"
/clone lib="FvI"
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
/note="Vector: pBlueScript II EcoRI;
/note="Vector: pBlueScript II SK(+) XR
/clone libe="Vector: pBlueScript II SK(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="fVIEA21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Gibberella
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                                                                         ĠĠĠĊĊĄŦĊĊĠĊĊĠĊĄĄĊĄĄĠĊĠĊĄĠĊĄĠĊĠĠĊĠĊŦĠŦĊĄĄĊĄŦĠĊĄĠĄ
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Pred. No. 9.5e-50;
); Mismatches 211;
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RESULT 12
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AUTHORS
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SOURCE
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VERSION
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                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 372; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
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                           194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1815 N. University St, Peoria, IL
Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIDX40TH
Seq primer: AAT TAA CCC TCA CTA A
                                                                                                                                                                                            74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 733)
Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L, Lee, Y., Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibberella
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EST1021027
CCTACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCG
                                                                 TCTACTCTTGGTGGTCTGATGGTGGTGGCTATGCCAACTACCGTATGGGTGAGGGAAGTC
                                                                                             ACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACCTACCCAACCTGGAAGGCGGCA
                                                                                                                                                   CCTCTGTCCTTGAGGCCCGCCAGGTCACCGGTAACTCTGAGGGTTACCACAACGGATACT
                                                                                                                                                                                          CCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATT
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                                                                                                                                                                                                                                                                                                                    /clone_Tib="FvI"
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site_2: XhoI; anamorph: Fusarium verticillioIdes. Library
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10e6 conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIzol. The cDNA was
directionally ligated into the pBlueScript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue type="mycelia"/clone_Tib="FvI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:117187"
/clone="FVIDX40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="m3125"
/db_xref="taxon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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                                                                                                                                                                                                                                                     32.5%;
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                                                                                                                                                                                                                                   <u>,</u>
                                                                                                                                                                                                                              Score 219.4; DB 8;
Pred. No. 9.5e-50;
D; Mismatches 211;
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moniliformis
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FVIDX40, mRNA
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JOURNAL COMMENT
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AUTHORS
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ORGANISM
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DR624376
LOCUS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 739)
Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Kendra, D.F., Town, C.D. and Whitelaw, C.A. Analysis of 87,000 expressed sequence tags reveals spliced introns in multiple genes of the fumonisis Unpublished (2005)
Contact: Brown, D.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
DR624376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Hypocreomycetidae; Hypocreales; Nectriaceae;
                                                                                                                                                                                                                                                                     Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIB280TH
Seq primer: AAT TAA CCC TCA C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                                                                Tel: 309 681 6230 Fax: 309 681 6689
                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Brown, USDA/ARS/NCAUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gibberella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR624376
EST1014504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCT 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTAGCTACCGAGGGATACCAGAGCAGTGGATCTTCTTCCATCTATGT 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGCGTCTACGGCTGGACCCGCAGCCCTCTCGTCGAGTACTACGTCATCGAGAACTACG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGCGGTCTACGGTTGGACCCCGCAACCCCGCTGGTCGAGTATTACATCGTCGAGAACTTTTG
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  /tissue type="mycelia"
/clone lib="FvI"
/clone lib="FvI"
/note="Vector: pBlueScript II SK(+) XR; Site_2: XhoI; anamorph: Fusarium verticil
FvI was prepared from growth on excised meroots and shoots. The roots and shoots we described above and then inoculated by di
                                                                                                                                   /strain="m3125"
/db_xref="taxon:117187"
/clone="FVIB280"
                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                               organism="Gibberella"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            moniliformis
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                                                                                                                                                                                          type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                    Peoria,
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Site 1: ECORI;
:illioTdes. Library
| maize seedling
| were prepared as
| dipping briefly in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACTACTATCAGA 680
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FVIB280, mRNA
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REFERENCE
AUTHORS
                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                            RESULT 14
DR625790
LOCUS
DEFINITION
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Best Local S
Matches 372
                                                                                                                                                     ORGANISM
                                                                              sequence.

DR625790

DR625790.1 GI:70700504

EST.

Gibberella moniliformis

M Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; So:

Hypocreomycetidae; Hypocreales; Nectriaceae; Gible 1 (bases 1 to 741)
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                                                                                                                                                                                                                                                                          DR625790
EST1015918
Kendra, D.F., Town, C
Analysis of 87,000
                      Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Kendra, D.F., Town, C.D. and Whitelaw, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n 32.5%;
Similarity 63.2%;
72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGCGTCTACGGCTGGACCCGCAGCCCTCTCGTCGAGTACTACGTCATCGAGAACTACG
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0; Mismatches 211;
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Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR
USDA
1815 N. University St, Peoria
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Tel: 309 681 6230
Fax: 309 681 6689
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TIGR sequence name: FVIBR33TH
Seq primer: AAT TAA CCT TCA CTA
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/clone lib="FvI"
/clone lib="FvI"
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site_2: XhoI; anamorph: Fusarium verticillioIdes. Library
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10e6 conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIzol. The cDNA was
directionally ligated into the pBlueScript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."
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ismatches 211;
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| р Q | ₽ 6 | Ş | Query Matc Best Local Matches 3 | ORIGIN | | PEATOKES | | | JOURNAL | TITLE | AUTHORS | REFERENCE | SOURCE ORGANISM | ACCESSION VERSION KEYWORDS | DEFINITION | RESULT 15 DR624330 | Db dd | φ | Db |
|--|--|---|--|--------|--|-----------------------|--|----------------|---|-------|----------------------------|--|---------------------------|--|--|-----------------------|---|---|--|
| 134 ACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAACCTGGAAGGCGGCA 193 | 154 CCTCTGTCCTTGAGGCCCGCCAGGTCACCGGTAACTCTGAGGGTTACCACAACGGATACT 213 | 74 CCACGGAGCTCGAAAAGCGACAGACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATT 133 | Match 32.5%; Score 219.4; DB 8; Length 763; ocal Similarity 63.2%; Pred. No. 9.6e-50; 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2; | | /clone="FVIB212" /tissue_type="mycelia" /clone_Tib="FvI" /clone_Tib="FvI" /note="Vector: pBlueScript II SK(+) XR; Site_1: EcoRI; /note="Vector growth on excised maize seedling roots and shoots. The roots and shoots were prepared as described above and then inoculated by dipping briefly in a suspension of 5 x 10e6 conidia per ml. The inoculated roots and shoots were then incubated on moistened Whatman #1 filter paper at room temperature under sterile conditions for 4 days. Fungal mycelial was collected, frozen in liquid nitrogen, ground to a powder, and then added to TRIzol Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml TRIzol. The cDNA was directionally ligated into the pBlueScript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)." | b Location/Qualitiers | USDA 1815 N. University St, Peoria, IL 61604, USA Tel: 309 681 6230 Fax: 309 681 6689 Email: browndw@ncaur.usda.gov TIGR sequence name: FVIB212TH Seq prime: AAT TAA CTA AAG GG. | USDA/ARS/NCAUR | spiiced introns in mulcipie genes of the fumonisin gene ciuscer Unpublished (2005) Contact: Brown, D.W. | alte | Proctor, R.H., Butchko, A. | EUKARYOTA; FUNGI; ABCOMYCOTA; PEZIZOMYCOTINA; SORGARIOMYCETEB; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella. 1 (bases 1 to 763) | moniliformis moniliformis | DR624330 DR624330.1 GI:70699012 EST. | DK624330 763 bp mRNA linear EST 11-JUL-2005 EST1014458 FvI Gibberella moniliformis cDNA clone FVIB212, mRNA | | 659 TTCTAGCTACCGAGGGATACCAGAGCAGTGGATCTTCTTTCATCTATGT 707 | 614 TCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 662 | 602 CTATCTTCAATGCTTGGGCTAATGCTGGCATGAGACTTGGAAACCACTATCAGA 658 |

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                                                    GCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCA 433
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Job time : 3419.97 secs

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8: /cgn2_6/ptodata/1/ina/PB_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*
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US-08-468-812-1
US-08-590-563-1
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US-08-768-373-3
US-09-047-370-18
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US-09-1849-242A-3
US-09-367-891A-1
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ALIGNMENTS

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COUNTRY: USA
ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REFERENCE/DOCKET NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324.204-US
TELEPAX: 212-867-0123
TELEFAX: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
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US-08-886-765-1
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Knap, Inge Helmer
TITLE OF INVENTION: Animal Fee
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58175000 No.
                                  FEATURE:
                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 405 Lex
CITY: New York
STATE: NY
NAME/KEY:
                                                  STRAIN:
                                                                     ORGANISM:
                                                  1: Thermomyces
DSM 4109
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Wagner, Peter
Mullertz, Anette
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N: Animal Feed
                                                                    lanuginosus
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US-09-115-660-1
US-09-115-660-1
; Sequence 1, Application US/09115660
; Patent No. 6245546
; GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
APPLICANT: Wagner, Peter
APPLICANT: Mullertz, Anette
APPLICANT: Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6245546disk of
STREET: 405 Lexington Avenue
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nes 675; Conserv
 STATE: N
COUNTRY:
ZIP: 101
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; NAME/KEY:
; LOCATION:
US-09-115-660-1
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.(
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,660
FILING DATE:
CLASSIFICATION NUMBER: US/09/115,660
FILING DATE:
PRIOR APPLICATION NUMBER: 08/886,765
FILING DATE:
APPLICATION NUMBER: 08/886,765
FILING DATE:
APPLICATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324.204-US
REFERENCE/DOCKET NUMBER: 4324.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Thermomyces
STRAIN: DSM 4109
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               GGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACC 540
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                                                                                                                                                                                                                                                                                                               CACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCAAC
                                                                 TGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGAC 480
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                                                      TGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGC
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Gaps

210 180 150 120 90

570

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Versio:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086.010-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1123 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-08-458-023B-3
                                                                                                                         US-08-458-023B-3
                                                            Query Match
Best Local S
Matches 391
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Patent No. 5667990
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Berka, Randy M.
APPLICANT: Yoder, Wendy
APPLICANT: Takagi, Shinobu
APPLICANT: Boominathan, Karuppan C
TITLE OF INVENTION: ASPERGILLUS EX
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56679900 No. 56679
                                                                                                                                                                                HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Humicola inso
                                                                                                                                                                                                                                                            TOPOLOGY: 11nea.
MOLECULE TYPE: DNI
MOLECULE TYPE: NO
                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 405 Lexis
CITY: New York
STATE: New York
                                                                                                                                     NAME/KEY:
                                                          / Match 35.4%;
Local Similarity 64.4%;
nes 391, Conservative
                                                                                                                                                                                                                                                                                                     TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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    CGTTCCTCGGGACAACTCGACGGCCCTTCAGGCTCGACAGGTGACCCCCAACGGCGAGGG
                            USA
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126..806
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                                                             0
                                                          Score 239; DB 2; 1
Pred. No. 3.2e-57;
0; Mismatches 210;
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EXPRESSION
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                                                                                       Length 1123;
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US-08-468-812-1
; Sequence 1, Ap
; Patent No. 593
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APPLICANT: Vehmaan
APPLICANT: M ntyl
APPLICANT: Fagerst:
APPLICANT: Lantto,
                                                                                                                                                                           APPLICANT: KILDU.,
APPLICANT: KILDU.,
TITLE OF INVENTION: Of Use
TITLE OF INVENTION: Of Use
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
CORRESSEB: STERNE, KESSI
COUNTRY: U.S.A.
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,812
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                  Washington
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Y: U.S.A.
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Kristo, Paula
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/ENTION: of Use
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/

US 08/332,412

FILING DATE: 31 CLASSIFICATION:

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US-08-468-812-1
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NAME: Bugaisky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
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APPLICATION NUMBER: US 0
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
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 ACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTTG
                                   CCATCGGCAACCACTTCGACGCCTGGGCCCGCGCCGCGTGAA----CCTGGGCAGCCACG
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Pred. No. 3.5e-45;
D; Mismatches 263
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US-08-590-563-1
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PRIOR APPLICATION NUMBER: US 08/468,812

APPLICATION NUMBER: US 08/468,812

FILING DATE: 06-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412

FILING DATE: 31-OCT-1994

CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001

FILING DATE: 29-JUL-1994

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2600
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Query Match
Best Local Similarity
Matches 396; Conserv
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COUNTRY: U.S.A.
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Suominen, Pirko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                         MOLECULE TYPE:
                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                           STRANDEDNESS: not TOPOLOGY: linear
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EDNESS: not relevant
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1100 New York Ave.,
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Fagerstr m, Richard
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Conservative
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59.0%;
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0
Score 196.2; DB 3;
Pred. No. 3.5e-45;
0; Mismatches 263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Secretion
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ACCGTCTCCATCA 996
                                   1375;
12;
Gaps
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RESULT 6
US-09-770-621-1
; Sequence 1, Ap;
; Patent No. 650
; GENERAL INFOR
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                                                                                                                 APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production as
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOSTREET: 1100 New York Ave., N.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                ADDRESSEE: STERN
STREET: 1100 New
CITY: Washington
                                                                                                                                                                                                                                                                                                                       1, Application (No. 6506593
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Suominen, Pirkko
Lahtinen, Tarja
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Vehmaanper , Jari
Fagerstr m, Richard
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                                                                                                                   GOLDSTEIN & FOX, N.W. Suite 600
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                                                                                                                                                                                      Secretion
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NAME/KEY:
LOCATION:
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Best Local S
Matches 396
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INFORMATION FOR SEO TO 25.086

REFERENCE/DOCKET NUMBER: 1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEO TO 2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DALE.
CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 31-OCT-1994
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                                                                                                                                                                                    305
                                                                                                                                                                                                                                                                                       529
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                                                    425
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96; Conservative
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                    ACGGGGGAACGTACGACATCTACGAGACCTGGCGGTACAACGCGCCG
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Pred. No. 3.5e~45;
0; Mismatches 263;
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Length Indels

1375; 12;

Gaps

ACCTACAAGGGCACCGTCACCACCG

GCCGGCAAGGGCT 588

1375;

12;

Gaps

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RESULT 7
US-09-235-832-1
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                                                                                APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
PRIOR APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, V

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
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APPLICANT:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER,
STREET: 1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF
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                   TOPOLOGY: 1
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                                                   TYPE: nucleic acid
STRANDEDNESS: No. (
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Suominen, Pirkko
Suominen, Tarja
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Vehmaanper , Jari
Fagerstr m, Richard
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                   linear
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                                                     Relevant
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; LOCATION:
US-09-235-832-1
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Best Local Similarity
Matches 396; Conser
                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: WATANABE, MANABU
                                                                                                                                                                                                                               Sequence
APPLICANT: MORIYA, TATSUKI
APPLICANT: AOYAGI, KAORU
APPLICANT: SUMIDA, NAOMI
APPLICANT: SUMIDA, NAOMI
APPLICANT: MURAKAMI, TAKESHI
TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE
TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM
TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
FILE REFERENCE: 99-0266*/LC(WMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07
                                                                                                                                                                                                                   No.
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Pred. No. 3.5e-45;
); Mismatches 263;
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AGCATCGACGGCA 484

705

588

MASS-PRODUCING

ACCGTCTCCATCA 996

NUMBER OF S SOFTWARE: P SEQ ID NO 8

OF SEQ ID NOS:

52

PatentIn Ver.

2.0

TYPE: DNA ORGANISM: TRICHODERMA VIRIDE MC300-1

DNA

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RESULT 9
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NAME/KEY: intro
LOCATION: (286)
FEATURE:
FEATURE: CDS
LOCATION: (413)
S-09-254-733-8
                                                                                                                                                Sequence 1, Application US/08121436A Patent No. 5837515
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Best Local Similarity
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NAME/KEY: 819_peptide
LOCATION: (14)..(112)
                                                                                      APPLICANT:
APPLICANT:
APPLICANT: Paloheimo, Marja
APPLICANT: Lahtinen, Tarja
APPLICANT: Fagerstr m, Richard
TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods
TITLE OF INVENTION: for Their Production
NUMBER OF SEQUENCES: 15
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                                                                                     Nevalainen, Helena
Saarelainen, Ritva
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Pred. No. 1.1e-44;
D; Mismatches 123;
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Best Local Similarity 68.:
Matches 278; Conservative
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARB: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,436A
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/F193/00221
FILING DATE: 24-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,893
FILING DATE: 29-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,308
APPLICATION NUMBER: US 07/524,308
APPLICATION INFORMATION:
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1015 base pair
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FEATURE:
NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/078,478
FILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA:
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ADDRESSEE: Sterne, K
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TELEPAX: (202) 3
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                                                                                                                                                                                                                                                                                                                                                              TARARARARGGGTCATCAACTTCTCGGGRARGCTACAACCCCCAACGGCAACAGCTACCTCT 605
                                                                                                                                                                                                                                                                                                                                                                                             TGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTG 316
                                                                                                                                                                                                                                       CCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCT 436
                                 ACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCG 616
                                                                                                                                             ACGACATTTACCGCACGCAGCGCGTCAACCAGCCGTCCATCATCGGCACCGCCACCTTTT 785
                                                                                                                                                                  ATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCTTCG 496
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join(176..448, 557..952)
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Pred. No. 1.7e-43;
0; Mismatches 125
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US-08-768-373-1
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                                                             ; FEATURE:
; NAME/KEY: exon
; LOCATION: 483..1039
; OTHER INFORMATION:
US-08-768-373-1
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Patent No.
Query Match 26.9%;
Best Local Similarity 65.4%;
Matches 283; Conservative
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V6

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/768,373

FILING DATE: 17-DEC-1996

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
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NAME/KEY:
LOCATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                         MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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                                                                                                                                            NAME/KEY: exon
LOCATION: 195..423
OTHER INFORMATION:
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10, 6228629
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T: 1100 NEW YORK AVENUE,
WASHINGTON
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LAHTINEN, TAKU-
: FAGERSTR M, RICHARD
: SUOMINEN, PIRKKO
: SUOMINEN, PIRKKO
TNVENTION: NOVEL XYLANASES, GENES EI
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M NTYL , ARJI
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 Score 181.8;
Pred. No. 3.8e
0; Mismatches
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  3; DB 3;
3.8e-41;
hes 147;
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                              Length 1281;
    Indels
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 Gaps
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US-09-849-242A-1
; Sequence 1, Application
; Patent No. 6635464
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: PALOH
; TINYOT.
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                                                                                           ZIP: 20005-3934

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vere
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,242A
FILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE,
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   APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
                                                                                                                                                                                                                                                                                         CITY: WASHINGTON STATE: DC
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                                                                APPLICATION NUMBER: US 0 FILING DATE: 17-DEC-1996
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FAGERSTRTM, RICHARD
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LANTTO, RAIJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAHTINEN,
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ATTORNEY/AGENT INFORMATION:

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RESULT 12
US-07-744-570B-1
US-07-744-570B-1
Sequence 1, Application US/07744570B
Patent No. 5202249
GENERAL INFORMATION:
APPLICANT: Kluepfel, D.
APPLICANT: Morosoli, R.
APPLICANT: Shareck, F.
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LOCATION: 483..1039

OTHER INFORMATION: /product= "
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-849-242A-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 283;
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Best Local
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REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1716.0540004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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LOCATION: 195..423
OTHER INFORMATION:
                                                                                                                                                                         CAATGTTGGCGGC
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llarity 65.4%;
Conservative
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202) 371-2540
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US-07-744-570B-1
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COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,!
FILING DATE: 19910813
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 675 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Single strand
TOPOLOGY: Circular
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Best Local Similarity 60.0%;
Matches 343; Conservative
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael J. Bradley
STREET: 1200 South 47th Street
STREET: Box Number 4023
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STATE: California
COUNTRY: United States
ZIP: 94804-0023
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                                                                                                  GCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTT
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 TATCAGAGCAGTGGAAGCTCGAACATCACGGT
                               TACTTCAGCAGCGGCTATGCTCGCATCACCGT
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                                                                   ĠĊĠĊĠĊĠĠĠĠĊAŤĠĂĂĊAŤĠĠĠĊĊAĠŢŦĊĄĠĠŤĂĊŤĂĆĄŢĠĂŤĊĄŤ
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Pred. No. 1.7e-37;
); Mismatches 211;
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                                                                     GCCACCGAGGGC 561
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RESULT

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; TOPOLOGY: 11:
; MOLECULE TYPE:
; FEATURE:
; FEATURE:
; NAME/KEY: CD
; LOCATION: jo
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REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3954.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
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Best Local Similarity
Matches 346; Conserv
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APPLICANT:
APPLICANT:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56935180 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/002,800 FILING DATE: 25-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/01
FILING DATE: 15-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy die
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TITLE OF INVENTION: ENZYMES WITH XYLANASE
TITLE OF INVENTION: ASPERGILLUS ACULEATUS
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                   257
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TGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAGCC----AAACGGCAACAGCTAC
                                                 ACAGCGTGACCTGGTCATCGGCCTCGAACTTCGTCGGTGGAAAGGGCTGGAACCCTGG-A
                                                                               ACGAGATCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGGCTGGAACCCCGGCC
                                                                                                                 GCTTCTGGACCGATGGCGCAAGCGGCGATGTTGAATACAGCAACGGCGCCGGGGGGGTCCT
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Andersen, Lene N
Si, Joan Q.
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ilarity 58.3%;
Conservative
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, 64th Floor
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RESULT 14
US-08-902-655A-5
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Patent No. 588500.
Patent No. 588500.
Patent No. 588500.
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Patent No. 588581
                                                                                                                                                                                            COUNTRY: United States of America ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,655A
FILING DATE: 30-July-1997
CLASSIFICATION: 435
                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Agris, Cheryl T.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                              TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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             SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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Mullertz, Anette
ENTION: ENZYMES WITH
FENTION: ASPERGILLUS
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Heldt-Hansen, Hans
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                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Kofod,
APPLICANT: Kauppin
APPLICANT: Christg
APPLICANT: Heldt-H
                                                                                                                                                                                                                                                 Sequence 5, Application US/09116622 Patent No. 6080567
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Best Local
APPLICANT: Kauppinen, Markus S.
APPLICANT: Christgau, Stephan
APPLICANT: Heldt-Hansen, Hans P.
APPLICANT: Dalboge, Henrik
APPLICANT: Dalboge, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: Si, Joan Q.
APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
APPLICANT: Munk, Niels
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE AC
TITLE OF INVENTION: ASPERGILLUS ACULEATUS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60805670 No. 6080567disk of
STREET: 405 Lexington Avenue, 64th Floor
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MOLECULE TYPE:
FEATURE:
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les 346; Conser
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Pred. No. 2.3e-36;
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   ATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTTGC 665
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FEATURE:
NAME/KEY:
LOCATION:
US-09-116-622-5
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FILING DATE: 16-July-1998

CLASSIFICATION: CLASSIFICATION: APPLICATION: AFFICATION: AFFICATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Agris, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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STATE: New York
COUNTRY: United States
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
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TOPOLOGY: li
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AACCATTTCAATGCCTGGGCGAAGCTGGGAATGAATCT---GGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCTATCGACTCGGCAAGACCACCTCGCGTCAACGCACCTAGCATCGA(
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                                                                                                             reccacriceacecrisecrisecriseringaarercaacecrise
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                                                                                                                                                                                                                                       TTCACGCAGTACTGGTCCATTCGCCAGACAAAGCGCGTCGGCGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAC
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Pred. No. 2.3e-36;
); Mismatches 239;
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    GCACAACTATCAG 669
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                                                                                                                 CACTACTACCAG 612
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                                                                                                                                                                                                                                       GTGACGACTGCC 612
                                                                                                                                                                                                                                                                                                   GTCCAGACGGGC 552
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Run

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Minimum
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Perfect score:
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9
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*
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Maximum Match 100%
Listing first 45 summaries
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7943.586 Million cell updates/sec
          US-09-467-368-1
US-10-237-386-9
US-09-803-454-3
US-10-425-115-177283
US-10-425-115-37173
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US-10-213-990-67
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US-11-018-645-21
US-09-790-070A-8
US-10-299-393-1
US-10-765-716-1
US-09-149-310-31
US-09-149-310-31
US-09-149-310-31
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     Sequence 1, Appli
Sequence 9, Appli
Sequence 3, Appli
Sequence 177283,
Sequence 82922, A
Sequence 68, Appl
Sequence 68, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 64, Appli
Sequence 71, Appl
Sequence 71, Appli
Sequence 70, Appl
Sequence 39, Appli
Sequence 1, Appli
Sequence 31, Appli
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Wagner, Peter Mullertz, Anette

Peter Kamp

Regult No.

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| / L . 0 | 1 | 71.8 | 71.8 | 71.8 | 71.8 | 72.4 | 72.4 | 72.4 | 72.4 | 72.4 | 72.4 | 78.4 | 78.4 | 80.8 | 82.6 | 82.6 | 83.6 | 89.4 | 90.2 | 94.2 | 101.8 | 103.6 |
| 10.0 | 3 | 10.6 | 10.6 | 10.6 | 10.6 | 10.7 | 10.7 | 10.7 | 10.7 | 10.7 | 10.7 | 11.6 | 11.6 | 12.0 | 12.2 | 12.2 | 12.4 | 13.2 | 13.4 | 14.0 | 15.1 | 15.3 |
| o # | | 642 | 642 | 642 | 642 | 1513 | 1513 | 744 | 744 | 663 | 663 | 628 | 591 | 539 | 642 | 642 | 394 | 972 | 561 | 561 | 643 | 2054 |
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| 08-10-637-386-10 | מר המני מון | US-10-626-724-12 | US-10-626-724-6 | US-10-626-583-12 | US-10-626-583-6 | US-09-909-207-11 | US-09-909-207-10 | US-09-909-207-5 | US-09-909-207-4 | US-09-909-207-2 | US-09-909-207-1 | US-11-018-645-10 | US-11-018-645-3 | US-10-437-963-15625 | US-10-626-724-4 | US-10-626-583-4 | US-10-425-115-48309 | US-11-018-645-19 | US-11-018-645-15 | US-11-018-645-13 | US-10-340-860A-39 | US-10-419-969-5 |
| sequence to, Appr | 5 | Sequence 12, Appl | Sequence 6, Appli | Sequence 12, Appl | Sequence 6, Appli | Sequence 11, Appl | Sequence 10, Appl | Sequence 5, Appli | 4 | 2 | Sequence 1, Appli | Sequence 10, Appl | Sequence 3, Appli | Sequence 15625, A | Sequence 4, Appli | Sequence 4, Appli | Sequence 48309, A | Sequence 19, Appl | • | Sequence 13, Appl | Sequence 39, Appl | Sequence 5, Appli |

ALIGNMENTS

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CITY: New York
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/467,368
FILING DATE: 21-Dec-1999
CLASSIFICATION NUMBER: US/09/467,368
FILING DATE: 1-JUL-1999
CLASSIFICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324.204-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
LENGTH: 983 base pairs
LENGTH: 983 base pairs
 MOLECULE TYPE: cD
ORIGINAL SOURCE:
ORGANISM: Th
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US20020160080Alo
STREET: 405 Lexington Avenue
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                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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; Sequence 9, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbesen, Ole
; APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Ali
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..705
; SEQUENCE DESCRIPTION: 1
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RESULT 3
US-09-803-454-3
; Sequence 3, Application US/09803454
; Publication No. US20030022280A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030022280A10zymes A/S
; APPLICANT: Takagi, Shinobu
; APPLICANT: Terui, Yuri
; APPLICANT: Terui, Yuri
; TITLE OF INVENTION: High Expression of Industrial Enz
; FILE REFERENCE: 6125.200-US
; CURRENT APPLICATION NUMBER: US/09/803,454
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 00:
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 00:
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Thermomyces lanugino US-10-237-386-9
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D; Mismatches 0;
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Enzymes

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RESULT 4
US-10-425-115-177283
; Sequence 177283, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
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TYPE: DNA

ORGANISM: Artificial S

PEATURE:

OTHER INFORMATION: Syr

JS-09-803-454-3
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Best Local S
Matches 485
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Local Similarity 72.0%;
hes 485; Conservative
                                                                                                                                                                                                                          199
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                                                                                                                                                                                                                                                                                                                                                          GTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                    GGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCAGCGGTACC
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Pred. No. 4.1e-107;
0; Mismatches 189;
                                             Molecules
                                             and
                                              Other
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; NUMBER OF SEQ ID NOS:
; SEQ ID NO 177283
; LENGTH: 850
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: CUS-10-425-115-177283
                                                                                                                                                      RESULT 5
US-10-425-115-82922
; Sequence 82922, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Mol
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/42
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 420; Conserv
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                                                                                                                                                                                                                                                                                TCGTCGCCACCGAGGGTTACTTCTCCTCCGGCAGCTCGTCGATCACC
                                                                                                                                                                                                                                                                                                    TCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTG 667
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                                                                                                                                                                                                                                                                                                                                                                       GCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGA 613
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                                                                                                                                                                                                                                                                                                                                                    CCCACTTCGACGCCTGGGCCTCCAAGGGCATGCAGCT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTACAAGATTGCGCAGACTCAGCGTGTCAACCAGCCCTCCATCGACGGCACCAAGACCT 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGCCATCTACGGCIGGACCCGCAACCCCCTTGTCGAGTACTACGTTGTTGAGAACTTTG 495
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ilarity 64.2%;
Conservative
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369326
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Pred. No. 7.6e-71;
); Mismatches 228;
                                                                       Molecules
                                                                       and
                                                                       Other
                                                                                                                                                                                                                                                                                                                                                    -CGGTCAGCACCAACTACCAGA 732
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                                                                      ules Associated With
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RESULT 6
US-10-425-115-37173
; Sequence 37173, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
pdf,ICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WUMBER OF SEQ ID NOS: 36932
SEQ ID NO 82922
LENGTH: 749
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(749)
OTHER INFORMATION: unsure
FEATURE:
OTHER INFORMATION: Clone II
US-10-425-115-82922
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Best Local Similarity 63.9%;
Matches 423; Conservative
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Pred. No. 1.7e-(
0; Mismatches ?
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; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Mol-
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21 (53222) B
; CURRENT APPLICATION NUMBER: US/10/42
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 37173
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT457
US-10-425-115-37173
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Best Local Similarity
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                        ACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 662
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llarity 62.5%;
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Pred. No. 1.6e-65;
); Mismatches 241;
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TCTÁTCÁCTGT 747
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RESULT 7
US-10-213-990-65
; Sequence 65, Application US/10213
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg

/10213990

```
## APPLICANT: Roemer, Terry
## TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUN
## TITLE OF INVENTION: ENZYMES AND METHODS OF USE
### FILE REFERENCE: 10182-019-999
### CURRENT APPLICATION NUMBER: US/10/213,990
### CURRENT FILING DATE: 2002-08-05
### NUMBER OF SEQ ID NOS: 72
### SOFTWARE: FASTSEQ for Windows Version 4.0
### SEQ ID NO 65
### TYPE: DNA
### ORGANISM: Aspergillus
### FEATURE:
### NAME/KEY: CDS
### LOCATION: (1)...(666)
### US-10-213-990-65
RESULT 8
US-10-213-990-68
; Sequence 68, A
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                                                                                                                                             GACCACTACTACCAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATC
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                                                                                    ACCGTTGCTGA
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  Application
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ilarity 61.5%;
Conservative
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  US/10213990
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Pred. No. 1.5e-60;
); Mismatches 249;
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GENERAL INFORMATE

GENERAL INFORMATE

APPLICANT: Bussey, Howard

APPLICANT: Storms, Reg

APPLICANT: Roemer, Terry

TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUM

TITLE OF INVENTION: ENZYMES AND METHODS OF USE

PILE REFERENCE: 10182-019-999

CURRENT APPLICATION NUMBER: US/10/213,990

CURRENT FILING DATE: 2002-08-05

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 68

LENGTH: 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LENGTH: 705
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(705)
US-10-213-990-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.8%;
Best Local Similarity 60.5%;
Matches 409; Conservative
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                                                                                                                                                                                                                                    GGGGCACTGTCAACACCGACGGTGGCACTTACAACATCTACACGGCC
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ATGCTCGCATCACCGT
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Pred. No. 1.4e-59;
D; Mismatches 249;
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RESULT 9
US-09-770-621-1
; Sequence 1, Ap
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                                                                                                                                                               ; NAME/KEY:
; LOCATION:
US-09-770-621-1
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                                                                                                                      Best
                                                                                                                                   Query Match
                                                                                                        Matches
                                                                                                                                                                                                                                                                                   TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 31-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 01
FILING DATE: 29-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: No. 1
TOPOLOGY: linear
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                                                                                                                      Similarity
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NVENTION: Production a
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Suominen, Pirkko
Suominen, Tarja
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Fagerstr m, Richard
Lantto, Raija
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                                                                                                     Score 196.2; DB 3;
Pred. No. 1.8e-51;
); Mismatches 263;
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                                                                                                                                                                                                                                                          Relevant
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                                                                                                      Gaps
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RESULT 10
US-10-286-993-1
; Sequence 1, Ap
; Publication No
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                                                                                    FILE REFERENCE: 1716.0340004

CURRENT APPLICATION NUMBER: US/10/286,993

CURRENT FILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: US/09/120,804

PRIOR FILING DATE: 1998-07-23

PRIOR APPLICATION NUMBER: PCT/F197/00037

PRIOR FILING DATE: 1997-01-24

PRIOR APPLICATION NUMBER: US 08/590,563

PRIOR FILING DATE: 1996-01-26

NUMBER OF SEQ ID NOS: 18
                                                      SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                   APPLICANT: Vehmaanpera, Jari
TITLE OF INVENTION: Production
TITLE OF INVENTION: Fungi
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APPLICANT: Paloheimo,
TYPE: DNA ORGANISM:
                                    ENGTH:
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  Actinomadura
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Lantrom, Richard
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Suominen, Pirkko
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RESULT 11

US-10-213-990-67

; Sequence 67, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGI
TITLE OF INVENTION: ENZYMES AND METHODS OF
FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; NUMBER OF SEQ ID NOS: 72
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; LOCATION: (303)..(1
; OTHER INFORMATION:
US-10-286-993-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.1%;
Best Local Similarity 59.0%;
Matches 396; Conservative
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Pred. No. 1.8e-51;
D; Mismatches 263;
                                                  METHODS OF USE
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; ORGANISM: Asperg:
US-10-213-990-67
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SEQ ID NO 67
LENGTH: 739
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Best Local Similarity
Matches 410; Conserv
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llarity 57.7%;
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RESULT 12
US-10-213-990-64
; Sequence 64, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUR
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-99
; CURRENT APPLICATION NUMBER: US/10/213,990
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|GCTGGAACCCTGGAAGCGCTAGGTACCGAGCTTTGTCAACGTCGGATGTGCAGACCTGTG 325
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Pred. No. 2.6e-49;
); Mismatches 248;
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                                                                               ENCODING INDUSTRIAL
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CURRENT FILING DATE: 2(
NUMBER OF SEQ ID NOS: 7;
SOFTWARE: FASTSEQ for W:
SEQ ID NO 64
LENGTH: 712
TYPE: DNA
ORGANISM: Aspergillus
US-10-213-990-64
Sequence 71, Application US/10213990

Publication No. US20030082595A1

GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF J
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US-10-213-990-71
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larity 57.7%;
Conservative
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Pred. No. 8.7e-47;
); Mismatches 253;
    METHODS OF USE
                  FUMIGATUS
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                  ENCODING
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Sequence 21, Application US/11018645; Publication No. US20050208178A1; GENERAL INFORMATION:
APPLICANT: Bauer, Michael
APPLICANT: Bedford, Michael
APPLICANT: Pulliam, Derrick
TITLE OF INVENTION: Microbially Expresse; TITLE OF INVENTION: Uses
FILE REFERENCE: 70357WOPCT; CURRENT APPLICATION NUMBER: US/11/018,64; CURRENT FILING DATE: 2004-12-20; PRIOR APPLICATION NUMBER: 60/531,404
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US-11-018-645-21
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FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(
IS-10-213-990-71
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CURRENT APPLICATION NUMBER: US/10/213,
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 71
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Best Local Similarity
Matches 340; Conserv
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nilarity 59.3%;
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Pred. No. 9.4e-42;
); Mismatches 221;
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RESULT 15
US-10-213-990-70

Sequence 70, Application US/10213990

Publication No. US20030082595A1

GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNTITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
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; NAME/KEY: CDS
; LOCATION: (1)..(978)
US-11-018-645-21
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Best Local
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NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21
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TYPE: DNA
ORGANISM: Artificial
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OTHER INFORMATION:
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Similarity 56.8%;
27; Conservative (
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Pred. No. 1.6e-38;
0; Mismatches 243;
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                                                           FUMIGATUS
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                                                           ENCODING
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; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 70
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Aspergillus
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Search completed: February 11, 2006, 23:51:28
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 1 US-11-170-653-9

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1 US-11-108-163B-5

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US-10-517-939-253

US-10-517-939-253

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- 2006 Biocceleration Ltd
Sequence 9, Appli
Sequence 231, App
Sequence 1, Appli
Sequence 5, Appli
Sequence 25, Appli
Sequence 25, Appli
Sequence 25, Appli
Sequence 165, App
Sequence 165, App
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Sequence 177, App
Sequence 195, App
Sequence 183, App
Sequence 217, App
Sequence 218, App
Sequence 219, App
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| 23 141.8 21.0 1077 7 US-10-517-939-181 24 131.2 19.4 1047 7 US-10-517-939-161 25 128 19.0 1029 7 US-10-517-939-219 26 127.8 18.9 747 7 US-10-517-939-227 27 124 18.4 1695 7 US-10-517-939-317 28 119.2 17.7 642 11 US-11-214-413-31 29 118 17.5 669 7 US-10-517-939-167 30 116.4 17.2 1086 7 US-10-517-939-205 31 114.8 17.0 1068 7 US-10-517-939-153 31 109.2 16.2 1020 7 US-10-517-939-153 32 109.2 16.2 1020 7 US-10-517-939-197 34 107.2 15.9 636 7 US-10-517-939-197 35 106.8 15.8 555 7 US-10-517-939-163 36 94.2 14.0 570 7 US-10-517-939-163 37 93.4 13.6 13.6 570 7 US-10-517-939-377 39 91.6 13.6 570 7 US-10-517-939-377 40 91.4 13.5 678 7 US-10-517-939-357 41 91.4 13.5 678 7 US-10-517-939-353 42 91 13.5 645 7 US-10-517-939-353 43 91 13.5 1053 7 US-10-517-939-353 44 90.2 13.4 570 7 US-10-517-939-375 45 89.8 13.3 1077 7 US-10-517-939-369 | | | | | | | | | | | | | | | | | | | | | | | |
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| .0 1077 .4 1047 .9 747 .4 1695 .7 669 .7 669 .2 1086 .0 1068 .1 633 .1 633 .9 636 .9 636 .0 570 .1 633 .9 636 .9 636 .9 636 .9 636 .9 636 .9 570 .1 1068 .1 1068 .1 1068 .1 1068 .2 1068 .3 1068 .4 1338 .5 1983 .5 1983 .7 1053 .7 1053 .7 7 7 | 89.8 | 90.2 | 91 | 91 | 91.4 | 91.4 | 91.6 | 91.8 | 93.4 | 94.2 | 106.8 | 107.2 | 108.4 | 109.2 | 114.8 | 116.4 | 118 | 119.2 | 124 | 127.8 | 128 | 131.2 | 141.8 |
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| US-10-517-939-181 US-10-517-939-219 US-10-517-939-219 US-10-517-939-317 US-11-214-413-31 US-10-517-939-211 US-10-517-939-211 US-10-517-939-211 US-10-517-939-207 US-10-517-939-207 US-10-517-939-207 US-10-517-939-251 US-10-517-939-367 US-10-517-939-367 US-10-517-939-377 US-10-517-939-377 US-10-517-939-379 US-10-517-939-379 US-10-517-939-379 US-10-517-939-379 US-10-517-939-379 US-10-517-939-379 US-10-517-939-379 US-10-517-939-379 US-10-517-939-379 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 11 | 7 | 7 | 7 | 7 | 7 |
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ALIGNMENTS

RESULT 1 US-11-170-653-9

Sequence 9, Application US/11170653
Publication No. US20050271769A1
GENERAL INFORMATION:

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APPLICANT: Danisco A/S

APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens

TITLE OF INVENTION: Xylanse Variants Having Alt
FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

CURRENT FILING DATE: 2005-06-23

PRIOR FILING DATE: 2002-09-09

PRIOR FILING DATE: 2002-09-09

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Patentin version 3.0

SEQ ID NO 9

LENGTH: 588

TYPE: DNA
ORGANISM: Thermomyces lanuginosus
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Best Local Similarity 100.0%; Pred. No. 4.7
Matches 582; Conservative 0; Mismatches
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GCAAGAGCCATC 183
                                                                        ATCAGCTGGGGA 123
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APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
ITTLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THE
ITTLE OF INVENTION: AND METHODS FOR MAKING AND USING THE
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
JUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 231
LENGTH: 1008
TYPE: DNA
ORGANISM: Bacteria
US-10-517-939-231
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Best Local Similarity 59.9%;
Matches 376; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Wu, Di
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 CAGGGCACCGTCTCCATGAACATGGGCTCCGGCGGTCAGTACAGCACCTCGTGGCGCAAC
                                   GGAGCGCAGGCCACGTACACCAACCTGGAAGGCCGCACCTACGAGATCAGCTGGGGAGAT
                                                                              GTCACGACCAACCAGGAGGGCACCAACAACGGCTACTACTACTCGTTCTGGACCGACAGC
                                                                                                     ACAACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGT
                                                                                                                                                           GTCGCGCTGGCGCGCTCGCCGCGCTGATGCTGCCGGGCACCCGCCCAGGCCGACACGGTC
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o. US20060003433A1
                                                                                                                                                                                                                                      Score 201.2; DB 7;
Pred. No. 1.1e-47;
D; Mismatches 243;
                                                                                                                                                                                                                                                                             Length 1008;
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APPLICANT: Suominen, Pirkko

ITITLE OF INVENTION: Method and DNA Constructs for Incre

ITITLE OF INVENTION: Carbohydrate Degrading Enzymes in

FILE REFERENCE: 1716.034000B/MAC/DJN

CURRENT APPLICATION NUMBER: US/11/108,163B

CURRENT FILING DATE: 2005-04-18

PRIOR APPLICATION NUMBER: US 60/562,692

PRIOR FILING DATE: 2004-04-16

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn version 3.3

SEQ ID NO 1
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                                                                                                                                      ; OTHER INFORMATION: Nf xynllA nucleotide sequence (AJ508952), the coding region is ; OTHER INFORMATION: from nt 303 to nt 1337 US-11-108-163B-1
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US-11-108-163B-1
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Publication No. US20060014247A1
GENERAL INFORMATION:
APPLICANT: Paloheimo, Marja
APPLICANT: Mantyla, Arja
APPLICANT: Leskinen, Sanna
                                                                 Query Match
Best Local Similarity
Matches 396; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                            TYPE: DNA
ORGANISM: Nonomuraea
FEATURE:
                                                                                                                                                                                                                                               LENGTH: 1375
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Kallio, Jarno
Puranen, Terhi
Lantto, Raij
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 TCGGCCTCCGGCGCATCGTCACCAGTGCCTTCGCCCTGGCACTCGCC
                        TCGGCTTTACCCCCGTTGCCCTTGCGGCCTTAGCCGGGACTGGGGCCCTGGCCTTCCCGG 64
                                                                                                                                                                                                               flexuosa
                                                                                  29.1%;
                                                                   Score 196.2; DB 11;
Pred. No. 3.1e-46;
); Mismatches 263;
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                                                                                                    Length 1375;
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 Arcécegrecec 408
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RESULT 4
US-11-108-163B-
                                         APPLICANT: Summinen, Pirkko

TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production |

TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi

FILE REFERENCE: 1716.034000B/MAC/DJN

CURRENT APPLICATION NUMBER: US/11/108,163B

CURRENT FILING DATE: 2005-04-18

PRIOR APPLICATION NUMBER: US 60/562,692

PRIOR FILING DATE: 2004-04-16

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.3

SEQ ID NO 5

LENGTH: 663

TYPE: DNA

ORGANISM: Nonomuraea flexuosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, App. Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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             PEATURE:
OTHER INFORMATION:
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Mantyla, Arja
Leskinen, Sanna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/11108163B No. US20060014247A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGAGGGTGGC 1007
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Lantto, Raij
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Kallio, Jarno
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             like
APPLICANT: Lantto, Raij

APPLICANT: Suominen, Pirkko

TITLE OF INVENTION: Method and DNA Constructs for Incre
TITLE OF INVENTION: Carbohydrate Degrading Enzymes in
FILE REFERENCE: 1716.034000B/MAC/DJN

CURRENT APPLICATION NUMBER: US/11/108,163B

CURRENT FILING DATE: 2005-04-18

PRIOR APPLICATION NUMBER: US 60/562,692

PRIOR FILING DATE: 2004-04-16

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.3

SEQ ID NO 4

LENGTH: 906

TYPE: DNA
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Mantyla, Arja
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Pagerstrom, Richard
Kallio, Jarno
Puranen, Terhi
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Lantto, Raij
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Pred. No. 2.4e-44;
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APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Wu, Di
APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS
TITLE OF INVENTION: AND METHODS FOR MAKING
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
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Best Loc
Matches
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APPLICANT: Steer, Brian
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SOFTWARE: FastSEQ for W
SEQ ID NO 225
LENGTH: 1059
TYPE: DNA
ORGANISM: Unknown
FEATURE:
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US-11-108-163B-3
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APPLICANT: Mantyla, Arja
APPLICANT: Leskinen, Sanna
APPLICANT: Fagerstrom, Richard
APPLICANT: Kallio, Jarno
APPLICANT: Kallio, Jarno
APPLICANT: Lantto, Raij
APPLICANT: Lantto, Raij
APPLICANT: Suominen, Pirko
TITLE OF INVENTION: Method and DNA Constructs
TITLE OF INVENTION: Carbohydrate Degrading En
FILE REFERENCE: 1716.034000B/MAC/DJN
CURRENT APPLICATION NUMBER: US/11/108,163B
CURRENT FILING DATE: 2005-04-18
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/11108163B Publication No. US20060014247A1 GENERAL INFORMATION:
APPLICANT: Paloheimo, Marja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 346; Conserv
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Mantyla, Arja
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Pred. No. 2e-43;
D; Mismatches 2:
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RESULT 8

US-11-108-163B-2

Sequence 2, Application US/11108163B

Publication No. US20060014247A1

GENERAL INFORMATION:
APPLICANT: Paloheimo, Marja
APPLICANT: Mantyla, Arja
APPLICANT: Fagerstrom, Richard
APPLICANT: Kallio, Jarno
APPLICANT: Evranen, Terhi
APPLICANT: Lantto, Raij
APPLICANT: Suominen, Pirko
TITLE OF INVENTION: Method and DNA Constructs for Inc
TITLE OF INVENTION: Carbohydrate Degrading Enzymes i
FILE REFERENCE: 1716.034000B/MAC/DJN
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PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3
LENGTH: 663
TYPE: DNA
ORGANISM: Nonomuraea flexuosa
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Best Local Similarity 61.5%;
Matches 354; Conservative
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Pred. No. 2e-43;
0; Mismatches 2
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US-11-108-163B-2
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Best Local S
Matches 354
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SEQ ID NO 2
LENGTH: 906
TYPE: DNA
ORGANISM: Nonomuraea flexuosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/11/108,163B
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US 60/562,692
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 25
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                                                                                             GGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAACGGAC
                                                                                                                                                CAGAAGCGGACCAGCGCACCATCACCATCGGCAACCACTTCGACGC
                                                                                                                                                                                                                         TACAACGCGCCGTCCATCGAGGGCACCCGGACCTTCCAGCAGTTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AACGCCTCCTTCAACCCGTCGGGTAACGCCTACCTCCACGCTCTACGG
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                                   AGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGC
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Pred. No. 2.2e-43;
); Mismatches 210;
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RESULT 9
US-10-517-939-165
; Sequence 165, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING
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MEHL

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RESULT 10
US-10-517-939-199
; Sequence 199, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
, APPLICANT: Wu, Di
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CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 165
LENGTH: 1047
TYPE: DNA
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Best Local S
Matches 340
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OTHER INFORMATION:
-10-517-939-165
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Pred. No. 4.4e-43;
0; Mismatches 215
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APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS
TITLE OF INVENTION: AND METHODS FOR MAKING
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 199
LENGTH: 1074
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ORGANISM: Unknown
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGGAGTGACGGTGGAGCGCAAGCCAACCTGGAAGGCGCACCTACGAGA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCGACAGAC-----AACCCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGCCTTAGCCGCGACTGGGCCCTGGCCTTCCCGGCAGGGAATGCCACGGAGCTCGAAA 88
                                                                                                                                                                                                                                                                                                                     ATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGAC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAACTGGAGCGGCATCAACAACTGGGTGGGCGGCAAGGGCTGGCAGACGGGCTCGTCCC 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAGCTGGGGAGATGGCGGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCGGCCTGAACG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGCGCAAACCTGCATCACGTCGAGCCAGACGGGCACCAACAACGGCAACTACTTTTCGT 145
                                                                                                                                                                                                                                                                                     GTCCGCCGGGTGGCCAGGGCTTCATGGGCACGGTGAACACCGACGGCGCCACGTACGACA 442
                                                                                                                                                                                                                                                                                                                                                                               ACGGTTGGACCCGCAACCCCGCTGGTCGAGTATTACATCGTCGAGAACTTTTGGCACCTATG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCT 322
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                                 CGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT
                                                                                              ACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTAC
                                                                                                                                           ACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCCACTTCG 562
                                                                                                                                                                                                                                               TCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCTTCGACCAAT 502
                                                                                                                                                                                                                                                                                                                                                            ACGGCTGGÁCCACCAATCCGCTCATCGAGTACTACATCGTCGACAAC
CCGAGGGCTACCAGAGCAGCGCAGCTCCGACATCACGGT
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                                                                     CCTGGGACAGCACAACTACCAGGTGATGGCCA 619
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AND USING
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                                                                                                       CAGATCGTTGCAA 622
                                                                                                                                                                                                                 GGGGCAGCTATC 382
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RESULT 11 US-10-517-939-255 ~~~~ance 255, Application

US/10517939

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APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 255
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; OTHER INFORMATION:
US-10-517-939-255
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Best Local Similarity
Matches 368; Conserv
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APPLICANT: Callen,
APPLICANT: Healey,
APPLICANT: Hazlewo
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TYPE: DNA
ORGANISM: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGCCTTAGCCGCGACTGGGGCCTTGGCCTTCCCGGCAGGGAATGCCCACGGAGCTCGAAAA
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CGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 662
                                                                                             ACTIGIAGCGTGCGGCAGTCGAAGCGCACCGGCGCATCACCACGGCCAACCACTTCA
                                                                                                                      ACTGGTCGGTCCGCCAGGACAAGCGCACCCAGCGGTACCGTCCAGACGGGCTGCCACTTCG
                                                                                                                                                         TCTATCGCACGCAACGGGTCAACCAGCCGTCGATCATCGGCACCGCGACGTTCTACCAGT
                                                                                                                                                                                         TCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGCACCCAAACCTTCGACCAAT
                                                                                                                                                                                                                        GTCCGCCGGGTGGCCAGGGCTTCATGGGCACGGTGAACACCGACGGCGCGCACGTACGACA
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                                                                                                                                                                                                                                                                                                                                                                                    CAAGAGCCATCCACTTTGAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCT
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                                ATGCCTGGGCCAGCCTCGGCATGAA----CCTGGGACAGCACAACTACCAGGTGATGGCCA
                                                             ACGCCTGGGCTCGCGCTGGTTTGAATGTCAACGGTGACCACTACTACCAGATCGTTGCAA
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Healey, Shaun
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Pred. No. 8.2e-39;
); Mismatches 260
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US-10-517-939-169
; Sequence 169, App
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APPLICANT:
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APPLICANT: Blum, David
APPLICANT: Bsteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 169
LENGTH: 1041
TYPE: DNA
ORGANISM: Unknown
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Obtained US-10-517-939-169
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                            ACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTGGTTTGAATGTCAA
                                                                                                       CAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACCAGCGGTACCGTCCAG 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGCAGGCCACGTACACCCAACCTGGAA 186
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                                                                                                                                                                                                                                                                                                 AACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACTGTCGAGTGCGAC 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCAACTACTTTTCCTTCTGGAAGGACAGCCCGGGTACCGTCAACTTCTGCATGTATGCC 171
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Healey, Shaun
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o. US20060003433A1
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Pred. No. 1.3e-
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CGGTGACCACTAC 606
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                                                                     CGGCACGATCACC 528
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SEQ ID NO 221
LENGTH: 1044
TYPE: DNA
ORGANISM: Unknown
FEATURE:
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APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS EN
TITLE OF INVENTION: AND METHODS FOR MAKING AND
PILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
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Best Local
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APPLICANT:
APPLICANT:
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                             464
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                                                                                                                                              GTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTTGGACCCGCAACCCGC
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                              ATCTAGGAACTGTCGAGTGCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCA
                                                                                                                                                                                             CGTTCAACTCGCC---CGGCAACGGCTACCTCACCCTGTACGGGTGGACCACGAATCCGC
                                                                                                                                                                                                                                                             ACTIGGGTGGGTGGCAAGGGCTGGCAGACCGGCTCGAATCGCACGGTGACCTACTCCGGTT
                                                                                                                                                                                                                                                                                     ACCTCGTCGGTGGAAAGGGCTGGAACCCCGGCCTGAACGCAAGAGCCATCCACTTTGAGG
                                                                                                                                                                                                                                                                                                                            CGGTGACCTTCTGCATGTATGCCAACGGCCGCTACACCTCCAACTGGAGCGGCATCAACA
                                                                                                                                                                                                                                                                                                                                                            AGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTA
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                                                               TGATCGAGTACTACATCGTCGACAGTTGGGGGCAGTTATCGACCGCCCGGCGGCCAGGGCT
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Wu, Di
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Healey, Shaun
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o. US20060003433A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 165.6; DB 7;
Pred. No. 1.4e-37;
0; Mismatches 234;
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                               523
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APPLICANT: Blum, David

APPLICANT: Esteghlalian, Alireza

TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THI

TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THI

FILE REFERENCE: 564462007901

CURRENT APPLICATION NUMBER: US/10/517,939

CURRENT FILING DATE: 2004-12-13

PRIOR APPLICATION NUMBER: PCT/US03/19153

PRIOR APPLICATION NUMBER: PCT/US03/19153

PRIOR APPLICATION NUMBER: 60/389,299

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from US-10-517-939-177
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Best Local S
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                                                                                                                                                                                                                                                                                    AGCTCAAATGCCACTGGAACCCAGAATGGTTACTACTATTCGTTTTGGAAGGATTCCGGT 147
                                                                                                                                                                                                                                                                                                             ACCCCCAACTCGGAGGGCTGGCACGATGGTTATTACTATTCCTGGTGGAGTGACGGTGGA 159
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 CCGCTGGTCGAGTATTACATCGTCGAGAACTTTGGCACCTATGATCC
                                             TCGGGCAGTTATAGCGCGAGTGGAACCAGCTACCTCGCACTTTACGGCTGGACTCGAAAC 324
                                                                               GAGGGTGTTTACCAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAAC 339
                                                                                                                                                               GGTAACCTCGTCGGTGGAAAGGGCTGGAACCCCCGGCCTGAACGCAAGAGCCATCCACTTT 279
                                                                                                                                                                                                                                             GCGCAGGCCACGTACACCAACCTGGAAGGCGGCACCTACGAGATCAGCTGGGGAGATGGC 219
                                                                                                                                                                                                                                                                                                                                                                     GCGATTGCTGCCGCAGCACTAGCGGTGGCGACTGTTCCAATCGCTCATGCGCAAACGCTT 87
                                                                                                                          AACAACTGGGTTGGCGGTAAAGGCTGGATGCCGGG---TACTCGGCGCACAGTCACCTAT 264
                                                                                                                                                                                                        AACGCCACCATGACACTCGGTGCCGGTGGAAACTATTCTTCATCCTGGAACAGCAGCACT 207
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Healey, Shaun
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o. US20060003433A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 165.4; DB 7;
Pred. No. 1.7e-37;
); Mismatches 266;
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       TCCTCCGGTGCT 399
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RESULT 15

US-10-517-939-195

US-10-517-939-195

Sequence 195, Application US/10517939

Publication No. US20060003433A1

GENERAL INFORMATION:

APPLICANT: Steer, Brian

APPLICANT: Callen, Walter

APPLICANT: Hazlewood, Geoff

APPLICANT: Hazlewood, Geoff

APPLICANT: Blum, David

APPLICANT: Blum, David

APPLICANT: Blum, David

APPLICANT: Bteeghlalian, Alireza

TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THE

TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE

FILE REFERENCE: 564462007901

CURRENT FILING DATE: 2004-12-13

PRIOR APPLICATION NUMBER: US/10/517,939

CURRENT APPLICATION NUMBER: BCT/US03/19153

PRIOR APPLICATION NUMBER: BCT/US03/19153

PRIOR APPLICATION NUMBER: BCT/US03/19153

PRIOR APPLICATION NUMBER: BCJ/US03/19153

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Best Local Similarity 59.0%;
Matches 333; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                      277
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TACATCGTCGAGAACTTTGGCACCTATGATCCTTCCTCCGGTGCTACCGATCTAGGAACT 414
                                                                                                                                                                                                    GGAAAGGGCTGGAACCCCGGCCTGAACGCCAAGAGCCATCCACTTTGAGGGTGTTTACCAG
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                                                                                         CCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCCGCTGGTCGAGTAT
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Pred. No. 3.3e-36;
); Mismatches 222;
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GACCTCACCGTGAGCGAAGGCAGC
                                                                                                                    GGCGGAACCATCACCACCGGCAACCACTTCGATGGCTGGGCGAGCTACGGCATGAA----C 570
                                                                                                                                      AGCGGTACCGTCCAGACGGGCTGCCACTTCGACGCCTGGGCTCGCGCTTGGATGTC 591
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Search completed: February 11, 2006, 22:06:17 Job time : 217.772 secs



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Run Title: Perfect score: US-09-467-368-2 1238 1 MVGFTPVALAALAA February 10, MVGFTPVALAALAATGALAF......VATEGYFSSGYARITVADVG 2006, 14:49:18;); Search time 151.432 (without alignments) 652.836 Million cell up

updates/sec

225

Scoring table: Sequence: BLOSUM62

Searched: 2443163 ведв, Gapop 10.0, Gapext 439378781 0.5 residues

Total number of hits satisfying chosen parameters:

Minimum Maximum 80 80 geq geq length: 2000000000

Post-processing: Minimum Maximum Listing Match 0% Match 100% first 45 summaries

Database 3: 1 A 9 2 3 5 4 A Geneseq 21:*
geneseqp1980s:*
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geneseqp2000s:*
geneseqp2001s:*
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Pred. score and is d. No. is the number of results predicted by chance to have re greater than or equal to the score of the result being p: is derived by analysis of the total score distribution. greater the s printed,

SUMMARIES

| 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | S | 4 | w | 2 | Ļ | Result No. |
|-------------------|----------|--------------------|--------------------|----------|--------------------|--------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|---------------|
| 663 | 671 | 678.5 | 681.5 | 684.5 | 684.5 | • | • | 688.5 | | • | • | • | 965 | 965 | 965 | 1083 | 1083 | 1083 | 1088 | 1238 | 1238 | 1238 | 1238 | Score |
| • | 54.2 | • | • | ٠ | • | • | | | 55.7 | • | 65.1 | 65.1 | 77.9 | 77.9 | 77.9 | 87.5 | 87.5 | 87.5 | | 100.0 | 100.0 | 100.0 | 100.0 | Query |
| 197 | 234 | 261 | 221 | 223 | 223 | 223 | 227 | 227 | 227 | 221 | 221 | | | | | | | | 194 | 225 | 225 | 225 | 225 | Length |
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| AAW60736 | ABB80186 | AAW18115 | ABB80185 | AAW67567 | AAR47122 | AAW57422 | AAR78231 | AAR75421 | AEB00301 | ADI66756 | AA018654 | AAB48548 | ADI66750 | AA018648 | AAB48542 | ADI66751 | AA018649 | AAB48543 | AAE18456 | AEB00305 | ABR63119 | AAW05187 | AAW01112 | ID |
| Aaw60736 Xylanase | | Aaw18115 Chaetomiu | Abb80185 A. fumiga | | Aar47122 pI 9.0 en | Aaw57422 Amino aci | Aar78231 Humicola | Aar75421 Humicola | Aeb00301 Xylanase | Adi66756 C. carbon | Aao18654 C carbonu | Aab48548 Cochliobo | Adi66750 P. variot | Aao18648 P varioti | Aab48542 Paecilomy | Adi66751 T. lanugi | Aao18649 T lanugin | Aab48543 Thermomyc | Aae18456 Thermomyc | Aeb00305 Xylanase | Abr63119 Thermomyc | Aaw05187 Endo-1,4- | Aaw01112 Xylanase. | Description |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|--|
| 640.5 | 640.5 | 643.5 | 643.5 | 643.5 | 643.5 | 643.5 | 643.5 | 644.5 | 644.5 | 644.5 | 646.5 | 646.5 | 647.5 | 647.5 | 662.5 | 663 | 663 | 663 | 663 | 663 | |
| 51.7 | 51.7 | 52.0 | | 52.0 | | | 52.0 | 52.1 | 52.1 | 52.1 | | 52.2 | | | 53.5 | | | | 53.6 | 53.6 | |
| 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 230 | 197 | 197 | 197 | 197 | 197 | |
| ហ | ഗ | 7 | 7 | 7 | 7 | 7 | 7 | ហ | ហ | ហ | ហ | Ç | 7 | 7 | N | œ | Ņ | ഗ | w | w | |
| AEB47001 | AEB47004 | AA030294 | AA030293 | AAO30283 | AAO30286 | AAO30284 | AAO30285 | AEB47006 | AAB18494 | AAE18496 | AEB47005 | AAE18492 | AAO30297 | AAO30298 | AAW18116 | ADI66745 | AAE18445 | AA018643 | AAB48537 | AAY98068 | |
| Aeb47001 | Aeb47004 | Aao30294 | Aao30293 | Aao30283 | Aao30286 | Aao30284 | Aao30285 | Aeb47006 | Aae18494 | Aae18496 | Aeb47005 | Aae18492 | Aao30297 | Aao30298 | Aaw18116 | Adi66745 | Aae18445 | Aao18643 | Aab48537 | Aay98068 | |
| Thermophi | Thermophi | Trichoder | Trichoder | Trichoder | Trichoder | Trichoder | Trichoder | Thermophi | Trichoder | Trichoder | Thermophi | Trichoder | Trichoder | Trichoder | Chaetomiu | S. commun | Schizophy | S commune | Schizophy | S. commun | |

ALIGNMENTS

RESULT 1
AAWO1112
ID AAWO
XX
AC AAWO
AC AA Xylanase 21-MAY-1997 AAW01112; AAW01112 standard; protein; 225 AA. (first entry)

plant Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermoascus; Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia; Byssochlamus; Paecilomyces; animal feed additive; in-vivo breakdown; cell wall; growth rate; feed conversion

Thermomyces lanuginosus.

WO9623062-A1

01-AUG-1996.

26-JAN-1996; 96WO-DK000046

26-JAN-1995; 95DK-00000094.

(NOVO) NOVO-NORDISK AS

Hansen PK, Wagner P, Muellertz P Knap IH;

N-PSDB; 1996-454790/45. DB; AAT40742.

Fungal xylanase prepns. construct for producing for use as animal feed additives recombinant Thermomyces xylanase and DNA

Claim Page 45-46; 69pp; English.

This sequence represents the xylanase from Thermomyces lanuginosus strain DSM 4109. This xylanase, and xylanases derived from Humicola, Thermoascus, Chaetomium, Mucor, Talaromyces, Malbranchea, Myceliophthora, Thielavia, Byssochlamus or Paecilomyces strains can be used in the monocomponent xylanase preparations of the invention. The xylanase preparations and the recombinant Thermomyces xylanase are useful as animal feed additives, which promote in-vivo breakdown of plant cell wall material and thus improve digestibility, growth rate and/or feed conversion hea, Myceliophthora,
e used in the
The xylanase
are useful as
of plant cell wall
und/or feed

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RESULT 2
AAW05187
XX AAW0
XX AAW0
XX AAW0
XX Endc
XX Endc
XX Endc
XX Endc
XX Fher
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XX Ther
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            The sequence represents an endo-1,4-beta-D-xylanase from Thermomyces lanuginosus (Humicola lanuginosa), which may be used as a breadimproving additive. The enzyme may be expressed recombinantly from a plasmid pYES2.0 vector in Saccharomyces cerevisiae DSM 10133 (claimed), and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour, optionally along with other enzymes (amylase, maltogenase, lipase, cellulase, hemicellulase, pentosanase, glucose- oxidase, laccase, protease and/or peroxidase). The enzyme combines particularly well with amylolytic enzymes, and may be used to improve baking properties of flour and/or dough, by increasing volume and improving texture, flavour, crumb softness, freshness and anti-staling properties, while improving dough machinability and stability. (Updated on 16-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endo-1,4-beta-D-xylanase; xylanase; Humicola lanuginosa; bread; enzyme; flour; baking; dough.
                                                                                                                                                                                                                                                                                                                                                                                             11-APR-1995;
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                                                                                                                                                                                                                                       Bread improving additive contg. xylanase from Thermomyces - and operation alpha-amylase, increases volume, improves anti-staling properties
                                                                                                                                                                                                                                                                                                                                 Jorgensen OB,
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22-FEB-1997
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   machinability field)
                                                                                                                                                                                                              Claim 4;
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                                                                                                                                                                                                             Page 31-32; 41pp;
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nilarity 100.0%;
Conservative 0
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Pred. No. 1.3e-108;
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RESULT 3
ABR63119
ID ABR6
XX ABR6
AC ABR6
XX Ther
XX XY1
OS Ther
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Best Local S
Matches 225
                The present sequence is the protein sequence of a thermostable xylanase of Thermomyces lanuginosus. The xylanase has a melting temperature (Tm) of 75.0 degrees C at pH 7.0. It is preferred for use in a claimed composition of the invention, which comprises at least 2 thermostable enzymes selected from an endoglucanase, xylanase, phytase, protease, galactanase, mannanase, dextranase and alpha-galactosidase. The composition is useful for improving the nutritional value of animal feeds, especially those containing soya, wheat, barley, oats and/or rye
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Peptide
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                                                                                                                                                                                                                                                                                                        Composition useful as an animal feed additive comprises thermostable enzymes selected from endoglucanase, xylana
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                                                                                                                                                                                                                                         Disclosure;
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Conservative (
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                                                                                                                                                                                                                                       Page 60-61;
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Pred. No. 1.3e-108;
; Mismatches 0;
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Best Local Similarity
Matches 225; Conser
                                                                        The invention relates to a process for preparing a mash (A) (having enhanced filterability and/or improved extract yield after filtration) which comprises preparing a mash in the presence of enzyme activities (comprising a xylanase of GH family 10 at at least 15% w/w of the total xylanase and endoglucanase enzyme protein) and filtering (A) to obtain a wort. Also described is a composition is useful for reducing the viscosity of an aqueous solution comprising a starch hydrolysate, which is a mash for beer making or a feed composition. The process is useful for the production of an alcoholic beverage, such as beer or whiskey and the composition is useful in the mashing and filtration step in brewing process. The present sequence represents a xylanase used in the mashing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparation of a mash (having enhanced filterability and/or improved extract yield after filtration) comprises preparing a mash in the presence of enzyme activities comprising xylanase of GH family 10 and filtering to obtain wort.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             xylanase; feedstuff; alcohol; fermentation; brewing; filtration.
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Pred. No. 1.3e-108;
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Query Match Best Local S Matches 194

Local Similarity mes 194; Conserv

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Score 1088; DB 5; Pred. No. 1.7e-94;); Mismatches 0;

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Best Local S
Matches 225
                                              The present invention relates to a modified xylanase exhibiting inc thermostability and alkalophilicity. Modified xylanase is useful in industrial process such as pulp manufacturing. Modified xylanase is useful for bleaching of pulp, processing of precision devices and improving digestibility of poultry and swine feed. Modified xylanase improved performance at conditions of high temperature and pH and exhibits improved thermophilicity and/or alkalophilicity in compari corresponding native xylanase. The present sequence is Thermomyces lanuginosus xylanase, Xyn
                                                                                                                                                                                                                                                                                                                                                                Modified xylanase exhibiting increased thermostability alkalophilicity useful for industrial processing e.g. 1 manufacturing.
      Sequence 194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-2002
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                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermomyces lanuginosus xylanase,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein;
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Pred. No. 1.3e-108;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xyn.
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ed; enzyme; Xyn.
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                                                                                                                              ied xylanase has
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                                                                                                                                                                                                      Query Match
Best Local S
Matches 193
                                                                                                                                                                                                                                                                                                                                                           The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non naturally occurring XA protein with enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring Bacillus circulans xylanase is used in an agent for bleaching pulp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermomyces
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                                                                                                                                                                                                      3 87.5%; Similarity 100.0%; Similarity 100.0%; Similarity 100.0%; Similarity O;
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                                                                                                  TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH
                              FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 16L; 114pp; English.
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                                                                                                                                                                                                      Score 1083; DB 3;
Pred. No. 5.1e-94;
D; Mismatches 0;
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TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH 92

TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGG

Best Matches

193;

Similarity

87.5%; llarity 100.0%; Conservative (

0;

Score 1083; DB 5; Pred. No. 5.1e-94; 0; Mismatches 0;

Length Indels

194;

<u>.</u>

Gaps

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Query Match

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RESULT 7
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                                                  The present invention relates to a non-naturally occurring xylanase activity (XA) protein comprising an amino acid sequence less than 97% conditions to a naturally occurring Bacillus circulans xylanase, where the protein has been modified to exhibit enhanced thermophilicity, conting a circulans xylanase, and has at least 5 amino acid substitutions. A circulans xylanase, and has at least 5 amino acid substitutions. A conditions in the bioconversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid covices and semiconductors. The present sequence is a xylanase protein conduction of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T lanuginosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 16L; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel xylanase activity in food and animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xylanase activity; enzyme; thermostable; xylanase; pulp liquid clarification; coffee extraction; plant oil extra starch extraction; food thickener; animal food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA018649
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  Sequence 194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bentzien J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermomyces lanuginosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (XENC-) XENCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xylanase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein, useful in bleaching process of pulp and industry, has enhanced thermostability and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194
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                                                       Query Match
Best Local S
Matches 193
                                                                                                                                                  xylanase from Bacillus circulans) protein appearing as ADI66730. Also included is a bleaching agent comprising the XA protein. The non-naturally occurring XA protein comprises at least four amino acid substitutions as compared to Bacillus circulans xylanase ADI66728. The amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64, 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30 or 144. The non-naturally occurring xylanase activity (XA) protein useful for bleaching pulp in the paper and related industries, but is also useful in the food and animal feed industries. The new protein is active at higher pH and temperature ranges than naturally occurring xylanases, simplifying incorporation of the xylanase treatment step pulp processing, especially where the enzyme is added after hot alkali treatment. The present sequence is a xylanase from another species included for comparison
                                                                                                                                                                                                                                                                                                                                  The invention relates to a mutant xylanase activity (XA, xylanase from Bacillus circulans) protein appearing as A
                                                                                                                                                                                                                                                                                                                                                                                                        New mutant xylanase (XA) protein comprising at least four amino aci substitutions as compared to Bacillus circulans xylanase, useful for bleaching (paper) pulp, and in the food and animal feed industries.
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ
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07-JUN-1999;
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                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bentzien J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T. lanuginosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xylanase; XA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (XENC-)
                                                      / Match 87.5%; Local Similarity 100.0%; 193; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     er industry; food; alkali treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XENCOR
               TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH
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                                                                                                                                            comparison.
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y; food; animal feed; thermostability; alkalinophilic;
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99US-0138156P.
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                                                                                                                                                                                                                                                                                                                                                                             24; 84pp; English.
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                                                      Score 1083; DB 8;
Pred. No. 5.1e-94;
0; Mismatches 0;
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                                                                                 Length 194;
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as ADI66730. Also
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                                                                                                                                                         Query Match
Best Local Similarity
Matches 169; Conserv
                                                                                                                                                                                                                                         The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacterial;
bleaching a
                                                                                                                                                                                                                                                                                                                                                                                       Non naturally occurring XA protein with enhanced thermoplalkalophilicity or thermostability relative to the natural Bacillus circulans xylanase is used in an agent for blead
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB48542
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                 153
RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNG
                                          TTPNSEGWHDGYYYSWWSDGGGDSTYTNNSGGTYEITWGNGGNLVGG
                                                                                                                    TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSGYARITVADVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVNAPSIDGTQTFDQYWSVRQDKRTSGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Bacillus circulans; xylanase; xylanase activi agent.
                                                                                                                                                                                                                                                                                                                                                           Fig 16K;
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-US013172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                      77.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194
                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                         Score 965; DB 3;
Pred. No. 7.5e-83;
L; Mismatches 13
                                                                                                                                                                                   Length
                                                                                                                                                           Indels
                                                                                                                                                                                                                                         bility relative to y be used as the bleaching pulp
                                                                                                                                                                                        _
                                                                                                     KGWNPGLNARAIH 61
                                                                                                                          KGWNPGLNARAIH 92
                                                                                                                                                                                                                                                                                                                                                                                                      hilicity,
ally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ty; XA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DHYYQIVATEGYF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECDGSIYRLGKTT
                                                                                                                                                                                                                                                                                                                                                                                         ching pulp.
HYYQIVATEGYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THYYOIVATEGYF 212
                                                                                                                                                           <u>,</u>
                                                                                                                                                         Gape
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RESULT 10
AAO18648
ID AAO18648
XX AAO18
AAO18648
DT 24-00
XX AV18
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XX Pae(
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                                                                                                                                                                 र्
                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a non-naturally occurring xylanase cc activity (XA) protein comprising an amino acid sequence less than 97% cc identical to a naturally occurring Bacillus circulans xylanase, where the protein has been modified to exhibit enhanced thermophilicity, cc alkalophilicity, or thermostability relative to naturally occurring B. cc circulans xylanase, and has at least 5 amino acid substitutions. A complete the bioconversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of cc wheat and corn for starch production, use as animal food additives to aid corn the digestibility of feedstuffs and in the washing of super precision cc described in the exemplification of the invention
                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 169; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P variotii xylanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA018648;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel xylanase activity in food and animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
liquid clarification; coffee extraction; plant oil extraction;
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bentzien J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-2000; 2000US-00710050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-2001; 2001WO-US048018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paecilomyces variotii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        extraction; food thickener;
                                                                                                             N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XENCOR INC
                                                                                                                                                                                                                                                                                                                                                194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RYNAPSIDGTQTFNQYWSVRQDKRSSGTVQTGCHFDAWASAGLNVTGDHYYQIVATEGYF
                               FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT
                                                                                                             TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSGYARITVADVG 194
  FTGVYQPNGTSYLSVYGWTRNPLVEYYIVENFGSSNPSSGSTDLGTVSCDGSTYTLGQST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 16K; 121pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dahiyat
                                                                                                                                                                                                                         77.9%;
llarity 87.6%;
Conservative 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein, useful in bleaching process of industry, has enhanced thermostability a
                                                                                                                                                                                                                         ; Score 965; DB 5; ; Pred. No. 7.5e-83 11; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             additive;
                                                                                                                                                                                                                                                                               Length 194;
                                                                                                                                                                                                                              Indels
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TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGG

FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTV

ECDGSIYRLGKTT 152 KGWNPGLNARAIH 61 KGWNPGLNARAIH 92 Query Match Best Local S Matches 169

Similarity

77.9%;
larity 87.6%;
Conservative 1:

Score 965; DB 8; Pred. No. 7.5e-83; 1; Mismatches 13

Length 194; Indels

Gaps

169;

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RESULT 11
AD166750
XX AD166
XX AD166
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                                       New mutant xylanase (XA) protein comprising at least fou substitutions as compared to Bacillus circulans xylanase bleaching (paper) pulp, and in the food and animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xylanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P. variotii xylanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADI66750;
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   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bentzien J,
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07-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paecilomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (XENC-) XENCOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alkali treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2004-118575/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        industry; food;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSGYARITVADVG
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       194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dahiyat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-00570856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variotii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0133714P
99US-0138156P
                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8; enzyme; bleaching; bleaching pulp;
animal feed; thermostability; alkalinophilic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225
                                                                                                                                                                                                                                                                                                                                                                                                                      84pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 least four amino acid xylanase, useful for mal feed industries.
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||||||||||
|HYYQIVATEGYF 181
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RESULT 12
AAB48548
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AC AAB48
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AC Cochl
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                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacterial; I bleaching a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non naturally occurring XA protein with enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring Bacillus circulans xylanase is used in an agent for bleaching pulp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (XENC-) XENCOR
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                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                    a 65.1%;
Similarity 67.9%;
50; Conservative 2
                                                                                                                                                         LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI
                                                                                                                                                                                                                                                                                                                                                                                                                              221
                                             VENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT
VENFGTYDPSSQSQNKGTVTSDGSSYKIAQSTRTNQPS
                                                                                                           GAGGSYS'
                                                                                                                                                                                                             MVSFTSIITAAVAATGALAAPATDVS-LVARQNTPNGEGTHNGCFWSWWSDGGARATYTN
                                                                                                                                                                                                                                                              MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATYTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 16Q; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              ξ,
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Pred. No. 9e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               identical to a naturally occurring Bacillus circulans xylanase, where the protein has been modified to exhibit enhanced thermophilicity, alkalophilicity, or thermostability relative to naturally occurring B. Circulans xylanase, and has at least 5 amino acid substitutions. A Circulans xylanase, and has at least 5 amino acid substitutions. A Cipulp, in the bioconversion of lignocellulosic materials to fuels, for Cipulp, in the bioconversion of lignocellulosic materials to fuels, for Ciproducing juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. Cimproving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid to the digestibility of feedstuffs and in the washing of super precision Ciproductors and semiconductors. The present sequence is a xylanase protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a non-naturally occurriactivity (XA) protein comprising an amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xylanase activity; enzyme; thermostable; xylanase; pulp liquid clarification; coffee extraction; plant oil extra starch extraction; food thickener; animal food additive;
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cochliobolus carbonum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel xylanase activity in food and animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bentzien J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA018654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carbonum xylanase
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                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                  GAGGSYSVSWGSGGNLVGGKGWNPG-TARTITYSGTYNYNGNSYLAVX
    VENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQ
                                                                                                                       LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAV)
                                                                                                                                                                                                                                               MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYS
                                                                                                                                                                                         MVSFTSIITAAVAATGALAAPATDVS-LVARQNTPNGEGTHNGCFWS
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                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                       65.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein, useful in bleaching process of pulp and industry, has enhanced thermostability and
                                                                                                                                                                                                                                                                                          Score 806.5;
Pred. No. 9e-6
%% Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s and starch, roducts, e.g. nd processing of d additives to aid f super precision ylanase protein
                                                                                                                                                                                                                                             WSDGGAQATYTN
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WSVRQDKRTSGT
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less than 97%
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      xylanase from Bacillus circulans) protein appearing as ADI66730. Also included is a bleaching agent comprising the XA protein. The non-naturally occurring XA protein comprises at least four amino acid substitutions as compared to Bacillus circulans xylanase ADI66728. The amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64, 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30 standard for bleaching pulp in the paper and related industries, but is also useful in the food and animal feed industries. The new protein is active at higher pH and temperature ranges than naturally occurring xylanases, simplifying incorporation of the xylanase treatment step intreatment. The prescribly where the enzyme is added after hot alkali treatment. The prescrib sequence is a xylanase from another species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAY-1999;
07-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. carbonum xylanase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mutant xylanase (XA) protein comprising at least four amino acid substitutions as compared to Bacillus circulans xylanase, useful for
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                                                                                                                                                                                                                                                                                                                    Sequence
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                              LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI
                                                                                                                                         MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATYTN
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GAGGSYSVSWGSGGNLVGGKGWNPG-TARTITYSGTYNYNGNS
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                                                                                                      MVSFTSIITAAVAATGALAAPATDVS-LVARQNTPNGEGTHNGCFWSWWSDGGARATYTN
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99US-0138156P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID NO 29; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 3.2.1.8; enzyme; bleaching; bleaching pulp;
food; animal feed; thermostability; alkalinophilic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pulp, and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
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67.9%;
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                                                                                                                                                                                                           Score 806.5; DB
Pred. No. 9e-68;
; Mismatches 4
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Best Local S
Matches 126
                                                                                                                                                                                                       process o
                                                                                                                                                                                                               The invention relates to a process for preparing a mash (A) (having enhanced filterability and/or improved extract yield after filtration) which comprises preparing a mash in the presence of enzyme activities (comprising a xylanase of GH family 10 at at least 15% w/w of the total xylanase and endoglucanase enzyme protein) and filtering (A) to obtain a wort. Also described is a composition is useful for reducing the viscosity of an aqueous solution comprising a starch hydrolysate, which is a mash for beer making or a feed composition. The process is useful for the production of an alcoholic beverage, such as beer or whiskey and the composition is useful in the mashing and filtration step in brewing process. The present sequence represents a xylanase used in the mashing
                                                                                                                                                                                                                                                                                                                                                                                                   presence of filtering
                                                                                                                                                                                                                                                                                                                                                                                                    Preparation of a mash (having enhanced filterability and extract yield after filtration) comprises preparing a mapresence of enzyme activities comprising xylanase of GH filtering to obtain wort.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-SEP-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzyme;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEB00301;
                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Festersen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-2004; 2004WO-DK000880
                                                                                                                                                                               Sequence
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                                                                                                                             l Similarity 55.8
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                                                                                                                                                                                                         of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VENEGTYDESSQSQNKGTVTSDGSSYKIAQSTRTNQESIDGTRTEQQ
                                             ATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGN
                                                                                          MVGFTPVALAALAATGALA-----FPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQ 55
                                                                                                                                                                                 227
                         VQYTNLEGSRYQVRWRNTGNFVGGKGWNPG-TGRTINYGGYFNPQGN
                                                                           MVSLKSVLAAATAVSSAIAAPFDFVPRDNSTALQARQVTPNAEGWHNGYFYSWWSDGGGQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MY.
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                                                                                                                                        55.7%;
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                                                                                                                              31;
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                                                                                                                             Score 689.5; DB 9;
Pred. No. 1.1e-56;
1; Mismatches 62;
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ash in the
family 10 and
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QTFDQYWSVRQDK 175
                         GYLAVYGWTRNPL 119
                                        SYLAVYGWTRNPL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ing; filtration.
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Title:
Perfect score:
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 Pred. No. 18 the number of results predicted by chance to have score greater than or equal to the score of the result being present is derived by analysis of the total score distribution.
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Score
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1238
1 MVGFTPVALAALAA
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3: pir3:*
4: pir4:*
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Maximum Match 100%
Listing first 45 summaries
MVGFTPVALAALAATGALAF......VATEGYFSSGYARITVADVG
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S71472
S43919
S71473
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T37005
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Biocceleration Ltd.
           endo-1,4-beta-xyla
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endo-1,4-beta-xyla
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xylanase 1 - fungu
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 |
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| 113 | 115 | 145 | 240.5 | 248 | 296 | 299.5 | 355.5 | 356 | 365 | 371 | 372 | 385 | 388 | 389.5 | 390 |
| 9.1 | 9.3 | 11.7 | 19.4 | 20.0 | 23.9 | 24.2 | 28.7 | 28.8 | 29.5 | 30.0 | 30.0 | 31.1 | 31.3 | 31.5 | 31.5 |
| 40 | 2817 | 50 | 266 | 809 | 607 | 607 | 802 | 209 | 781 | 954 | 229 | 211 | 211 | 789 | 211 |
| N | N | N | μ | N | N | N | N | N | N | μ | N | ۲ | μ | Ŋ | N |
| PQ0202 | B97033 | A61149 | S48865 | B53295 | S24754 | S49528 | A36910 | JC4909 | S51592 | S20907 | S39155 | S48229 | JC1198 | S58235 | 849542 |
| | | | | | | | | | | | | | | | ø. |
| endo-1,4-beta-xyla | uncharacterized pr | endo-1,4-beta-xyla | endo-1,4-beta-xyla | xylanase (EC 3.2.1 | endo-1,4-beta-xyla | endoxylanase - rum | xylanase, beta(1,3 | endo-1,4-beta-xyla | XynB precursor - R | endo-1,4-beta-xyla | xylanase 2 - fungu | endo-1,4-beta-xyla | endo-1,4-beta-xyla | endo-1,4-beta-xyla | endo-1,4-beta-xyla |

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A;Introns: 81/2
C;Function:
A;Pathway: xylan degradation
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase
C;Keywords: glycosidase; hydrolase; polysaccharide degradatior
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-219/Product: endo-1,4-beta-xylanase A #status experimenta
F;42-219/Domain: endo-1,4-beta-xylanase homology <XYL>
F;115,206/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: xylanase A
C;Species: Chaetomium gracile
C;Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_char
C;Accession: S71472; S78206
R;Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi,
Curr. Genet. 29, 73-80, 1995
A;Title: Two family G xylanase genes from Chaetomium gracile
A;Reference number: S71472; MUID:96118924; PMID:8595661
A;Accession: S71472
A;Molecule type: DNA
A;Residues: 1-219 <YOS>
A;Residues: 1-219 <YOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
S71472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 31-45;82-94;152-160 <YOH>
A;Cross-references: UNIPARC:UPI0000175A79;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q12579; UNIPARC:UPI00000421A6; A;Accession: S78206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endo-1,4-beta-xylanase (EC 3.2.1.8)
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Best Local :
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                                                                                                                                                                                                                                                                                                                             Local Similarity nes 133; Conserv
 176
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                                                                                                                                                                                                                                                                                      μ
                                                                                                                                                                                                                                                                MVGFTPVALAALAATGALAFPAGNAT---ELEKRQTTPNSEGWHDGYYYSWWSDGGAQAT 57
                                                                           YXIVESFGTYDPSSQASKFGTIQQDGSTYTIAKTTRVNQPSIEGTST
                                                                                                                                                          SGSVNVAAHFNAWAQAGLKL-GSHNYQIVATEGYQSSGSSSITVS
                                SGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVA
                                                                                                   YYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQT
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59.1%; Pr
tive 29;
                                                                                                                                                                                                                                                                                                                           Score 691.5; DB 2;
Pred. No. 5.3e-48;
9; Mismatches 54;
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TFDQFWSVRQNHRS 175
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                                                                                                                                                                                                                                                                                                                                                                       219;
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N

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***, Dalboge, H.; Heldt-Hansen, H.P.

Mol. Gen. Genet. 243, 253-260, 1994

A; Title: A novel method for efficient expression cloning of fungal enzym

A; Reference number: $43919; MUID:94247364; PMID:8190078

A; Accession: $43919

A; Molecule type: mRNA

A; Cross-references: UNIPROT:P55334; UNIPARC:UPI0000421A4; EMBL:X76047; N.

C; Genetics:

A; Gene: XYL1

C; Function:

A; Pathway: xylan degradation

C; Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C; Keywords: glycosidase; hydrolase; polysaccharide degradation

F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 48-225/Domain: endo-1,4-beta-xylanase; #status predicted <SIG>
F; 112,123,157/Binding sit--

F; 121,212,77-
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endo-1,4-beta-xylanase (EC 3.2.
C;Species: Humicola insolens
C;Date: 19-Mar-1997 #sequence_r
C;Accession: S43919
R;Dalboge, H.; Heldt-Hansen, H.
Mol. Gen. Genet. 243, 253-260,
                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-241 < YOS>
A; Cross-references: UNIPROT:Q12580; UNIPARC
A; Accession: $78207
A; Molecule type: protein
A; Residues: 38-44; 89-91; 153-161 < YOH>
A; Residues: UNIPARC:UPI0000175A77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
S71473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;YOShino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, Curr. Genet. 29, 73-80, 1995
A;Title: Two family G xylanase genes from Chaetomium gracile A;Reference number: S71472; MUID:96118924; PMID:8595661
A;Accession: S71473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endo-1,4-beta-xylanase (EC 3.2.1.8) B p C;Species: Chaetomium gracile C;Date: 09-Dec-1997 #sequence_revision C;Accession: S71473; S78207 M;Accession: S71473; S71473 M;Accession: S71473; S71473 M;Accession: S71473 M;Accessi
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Best Local S
Matches 126
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                      ;Pathway: xylan degradation
;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
;Keywords: glycosidase; hydrolase; polysaccharide degradation
;1-30/Domain: signal sequence #status predicted <SIG>
;31-241/Product: endo-1,4-beta-xylanase B #status predicted <MAT>
                                                                                                                                                                                                      Function:
                                                                                                                                                                                                                                                Introns: 88,
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126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVGGSVNMQNHFNAWQQHGMPL-GQHYYQVVATEGYQSSGESDIYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITV
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Pred. No. 8e-48;
L; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNIPARC: UPI00000421AB;
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site: Glu #status predicted

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A; Molecule type: DNA
A; Residues: 1-223 <SAA>
A; Cross-references: UNIP
A; Experimental source: st
A; Accession: S39884
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C;Species: T
C;Date: 19-M
                                                                                                                                                                                                                                            A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-33/Domain: propeptide #status predicted <PRO>
F;34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>
F;45-223/Domain: endo-1,4-beta-xylanase homology <XYL>
F;71,94/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;110,121/Binding site: substrate (Tyr) #status predicted
F;119,210/Active site: Glu #status predicted
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S39883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 34-43;49-57;121-151;178-191 <SAF>
A; Cross-references: UNIPARC: UPI0000175A7C; UNIPARC: UPI0000175
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C;Date: 19-Mar-1997 #sequence_revision
C;Accession: S39883; S39884
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C; Function:
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Genet. 241, 497-503, 1993
Cloning, sequencing and enhanced expression of
ce number: S39883; MUID:94088442; PMID:8264524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
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                                                                                                                 MVNFSSLFLAASAAVVAVAAP-GELPGMHKRQTLTSSQTGTNNGYYY
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SSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTS 178
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anase II
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                                                                                                                                                                                              Score 684.5; DB Pred. No. 2e-47;
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Pred. No. 9.4e-48;
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QFWSVRQNKRSGG 178
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SFWTDGQGNVQYT 59
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homology

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RESULT 5

S57477
endo-1,4-beta-xylanase (EC 3.2.1.8) 1 precursor - Emerically in the Emerical State of the C; Species: Emerically inidulans, Aspergillus nidulans C; Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text C; Accession: S57477
R; Perez-Gonzalez, J.A.
submitted to the EMBL Data Library, June 1995
A; Description: Expression in Saccharomyces cerevisiae of A; Reference number: S57469
A; Accession: S57477
A; Molecule type: Data Library
                                                                                             xylanase 1 - fungus (Trichoderma reesei)
C;Species: Trichoderma reesei
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #t(
C;Accession: S39154
R;Toerroenen, A.; Mach, R.L.; Messner, R.; Gonzalez, I
Biotechnology 10, 1461-1465, 1992
A;Title: The two major xylanases from trichoderma rees
A;Reference number: S39154
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-225 <PER>
A;Cross-references: UNIPI
C;Genetics:
A;Introns: 93/2
C;Function:
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Best Local S
Matches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description: catalyzes the hydrolysis of 1,4-beta-xylosidic l;Pathway: xylan degradation;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase l;Keywords: glycosidase; hydrolase; polysaccharide degradation;1-19/Domain: signal sequence #status predicted <SIG-1,20-225/Product: endo-1,4-beta-xylanase l #status predicted <N-1,4-225/Domain: endo-1,4-beta-xylanase homology <XYL>1,121,212/Active site: Glu #status predicted
                                  Genetics:
                                                                                                                                                                                                                                                                                       σ
                                               references: UNIPROT: P36217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                         SKRTGGTVTTANHFNAWAALGMRL-GTHNYQIVATEGYQSSGSASITV
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                                                                <TOE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 680.5; DB 1; ; Pred. No. 4.1e-47; 31; Mismatches 57;
                                               UNIPARC: UPI00000421A9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIPARC: UPI0000139073;
                                                                                                                                                                                   Gonzalez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerevisiae
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                                                                                                                                                                                                                  #text_change
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                                                                                                                                                    characterization
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                                               EMBL: X69573;
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                                               NID: g396563;
                                                                                                                                                                                   Harkki,
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A; Molecule type: protein
A; Residues: 1-197 <OKU>
A; Cross-references: UNIPAF
A; Experimental source: ATC
C; Function:
                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 1-27 < PAI>
A; Cross-references: UNIPARC: UPI0000172967
R; Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk,
FEBS Lett. 334, 296-300, 1993
A; Title: Amino acid sequence and thermostabil
A; Reference number: $38973; MUID: 94063044; PN
A; Accession: $38973
                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 83-123 < BRA>
A; Cross-references: UNIPARC: UPI0000172966
R; Paice, M.G.; Jurasek, L.; Carpenter, M.R.;
Appl. Environ. Microbiol. 36, 802-808, 1978
A; Reference number: A05147; MUID: 79102289; PN
A; Accession: A05147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endo-1,4-beta-xylanase (EC 3.2.1.8) N;Alternate names: xylanase A C;Species: Schizophyllum commune C;Date: 27-Jun-1994 #sequence_revis: C;Accession: A44597; S41411; A05147
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase
C;Keywords: extracellular protein; glycosidase; hydrolase; po:
F;12-197/Domain: endo-1,4-beta-xylanase homology <XYL>
F;87,184/Active site: Glu #status predicted
F;111-160/Disulfide bonds: #status experimental
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A44597
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Eur. J. Biochem. 219, 821-827
A;Title: Identification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 1-197 <YAG>
A;Residues: 1-197 <YAG>
A;Cross-references: UNIPROT:P35809; UNIPARC:UPI0000034D33
A;Experimental_source: strain Delmar ATCC 38548
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les 128; Conserv
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                                                                                                                     catalyzes
                                                                                                                                                               source: ATCC 38548
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A05147; S38973
                                                                                                                     hydrolysis
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Pred. No. 4.8e-46;
2; Mismatches 60
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lysaccharide degradation
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YQYWSVRRNHRSS 179
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SVYGWSRNPLIEY 119
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                                                                                                                       bonds in xylans
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                                                                                                                                                                                                                                                                                                                            Yaguchi, M.; Jurasek, L.;
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endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae
N;Alternate names: endo-1,3-beta-xylanase G2; xylanase G2
C;Species: Aspergillus oryzae
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change
C;Accession: JC7577; PC7120
R;Kimura, T.; Suzuki, H.; Furuhashi, H.; Aburatani, T.; Morimot
Blosci. Biotechnol. Biochem. 64, 2734-2738, 2000
A;Title: Molecular cloning, overexpression, and purification of
A;Reference number: JC7577
A;Accession: JC7577
A;Accession: JC7577
A;Cross-references: UNIPROT:Q9HFA4; UNIPARC:UPI000069976; DDBJ
A;Experimental source: strain KBN616
A;Accession: PC7120
A;Accession: PC7120
A;Accession: PC7120
A;Accession: PC7120
A;Cross-references: UNIPARC:UPI0000175A84
C;Comment: This enzyme has strong similarity to other fungal fa
C;Genetics:
A;Gene: xynG2
A;Introns: 100/2
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase h
C;Keywords: glycosidase; hydrolase
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endo-1,4-beta-xylanase (EC 3
N;Alternate names: xylanase
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                                                                                                                                                                                                                                        WSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVY
                                                                                                                                                                                                                                                                      MVSFSSILLACSAAIGALATPIEPLADHPNEAFNETAFNDLVGRSTPSSTGYNNGYYYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RYNAPSIDGTQTFEQFWSVRNPKKAPGGSISGTVDVQCHFDAWKGLGMNLGSEHNYQIVA
                                                                                                                    WSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITV
                                                                                                                                                  GWTTDPLIEYYIVESYGTYNPGSGGTYKGQVTSDGGTYNIYTSVRTNAPSIIGTATFTQF
                                                                                                                                                                                                             WTDGGGDVTYTNGNGGSYSVQWSNVGNFVGGKGWNPG-SSRAITYSGSFNPSGNGYLAVY
                                                                                                                                                                                                                                                                                                  MVGFTPVALAALAATGALAFP-----
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61.3%;
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                  1.8)
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                                                                                                                                                                                                                                                                                                                                Score 659; DB 2;
Pred. No. 2.2e-45;
0; Mismatches 61
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Pred. No. 8.8e-46;
                  N
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                 precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aburatani, T.; Morimoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SGTVQTGCHFDAWARAGLNVNGDHYYQIVA
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                                                                                                                                                                                                                                                                                                   -AGNATELEK--ROTTPNSEGWHDGYYYSW
                  Emericella
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A; Cross-references: UNIPROT: P55333; UNIPARC: UPI0000139075; EME C; Genetics:
A; Introns: 89/3
C; Function:
A; Description: catalyzes the hydrolysis of 1,4-beta-xylosidic A; Description: catalyzes the hydrolysis of 1,4-beta-xylosidic A; Pathway: xylan degradation
C; Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-19/Domain: signal sequence #status predicted <SIG>
F;19-221/Product: endo-1,4-beta-xylanase 1 #status predicted <F;44-221/Domain: endo-1,4-beta-xylanase homology <XYL>
F;117,208/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Emericella nidulans, Aspergillus n
C;Date: 10-Oct-1995 #sequence_revision 22-Nov
C;Accession: S57469
R;Perez-Gonzalez, J.A.
submitted to the EMBL Data Library, June 1995
A;Description: Expression in Saccharomyces ce
A;Reference number: S57469
A;Accession: S57469
A;Molecule type: DNA
A;Residues: 1-221 <PER>
                                                                                                                                                                                                                                                                                                                                                R; Yaguchi, M.
submitted to the Prof
A; Reference number: 1
A; Accession: A44593
                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 1-190 < YAG>
A; Cross-references: UNIPARC: UPI00000493CB
A; Experimental source: strain E58
R; Campbell, R.L.; Rose, D.R.
submitted to the Brookhaven Protein Data Bank,
A; Reference number: A52868; PDB: 1XND
A; Contents: annotation; X-ray crystallography,
                                                                                                                                                                                                                                                                                                                                                                                                                            endo-1,4-beta-xylanase (EC 3.2.1 N;Alternate names: xylanase C;Species: Trichoderma harzianum C;Date: 27-Jun-1994 #sequence_rev C;Accession: A44593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
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A44593
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                                                                        A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
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Best Local Similarity
Matches 122; Conser
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10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
                   Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177
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                                                                                                                                                         catalyzes
                                                                                                                                                                                                                                                                                                                                                                       Protein Sequence
er: A44593
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                                                           Glu
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 51.4%;
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Pred. No. 1.
Score
Pred.
                                                        experimental
                                                                                                                                                                                                                                                                                                                                                                                            Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [validated]
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lysaccharide degradation
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   No.
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es cerevisiae
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ches 59;
   .5; DB 1;
1.1e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YYYSWWSDGGAQA 56
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                   190;
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                                                                                                                                                         bonds in xylans
                                                                                                                                                                                               residues 1-46,'A'48-190
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Local

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RESULT 11
A44595
endo-1,4-beta-xylanase (BC 3.2.1.8) IIB (proteinase-sensitive) - fungus (Tz endo-1,4-beta-xylanase IIB
C;Species: Trichoderma viride
C;Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: A44595
R;Yaguchi, M.
submitted to the Protein Sequence Database, March 1994
A;Reference number: A44593
A;Accession: A44595
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-190 <YAG>
A;Cross-references: UNIPROT:Q7M520; UNIPARC:UPI0000172968
C;Function:
A;Description: catalyzes the hydrolysis of 1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;12-190/Domain: endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; Glu #status predicted
F;126-127/Cleavage site: Glu #status predicted
F;127-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicte
RESULT 12
A44594
endo-1,4-beta-xylanase (EC 3.2.1.8) IIA -
N;Alternate names: xylanase IIA
C;Species: Trichoderma viride
C;Date: 27-Jun-1994 #sequence_revision 22
C;Accession: A44594
R;Yaguchi, M.
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.5; Conservative
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                                                                                                                                                                                                                                                                                                                                                               QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI
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|::|||||||||||:|:|:||
QTIGPGTGYSNGYYYSYWNDGHAGVTYTNGGGGGSFTVNWSNSGNFVGGKGWQPGTKNKVI
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                                                                                                                                                             FSSGSASITVS
                                                                                                                                                                                        FSSGYARITVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSSGYARITVA 222
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 636.5; DB 1 Pred. No. 1.1e-43;
                                                                              IIA
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                                 22-Nov-1996
                                                                            fungus
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                                                                              (Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                48;
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                            #text_change
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                                 09-Jul-2004
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ঠ
                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 32-51 <KI2>
A;Cross-references: UNIPARC:UPI0000175A85
C;Genetics:
A;Gene: xynA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic b A;Pathway: xylan degradation C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase h C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;12-190/Domain: endo-1,4-beta-xylanase homology <XYL>F;77,88/Binding site: substrate (Tyr) #status predicted F;86,177/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kimura, T.; Ito, J.; Kawano, A.; Makino, Biosci. Biotechnol. Biochem. 64, 1230-1237, A;Title: Purification, characterization, and A;Reference number: JC7307
A;Accession: JC7307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endo-1,4-beta-xylanase (EC 3.2.1.8) - Penicillium s N;Alternate names: endo-1,3-beta-xylanase; xylanase C;Species: Penicillium sp. C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 C;Accession: JC7307; PC7086
                                                                   В
                                                                                                                                                                                                           A;Introns: 89/2
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase
C;Keywords: glycoprotein; glycosidase; hydrolase
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                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: A;Accession: PC7086
                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-221 <KIM>
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C;Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                         Query Match
Best Local S
Matches 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Function:
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Best Local (
                                                                                                                                                          Local Similarity
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                            NLEGGTYBISWGDGGNLVGGKGWNPGLNARAIHFBGVYQPNGNSYLAVYGWTRNPLVBYY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 151
                                                                                        MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSE-GWHDGYYY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRVNQPSIIGTSTFYQYWSVRRTHRSSGSVNTANHFNAWAQQGLTL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTIGPGTGENNGYEYSYWNDGHGGVTYTNGPGGQFSVNWSNSGNEVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 91
                                                                                                                                        48.4%;
llarity 51.1%;
Conservative 4
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                                                                                                                                        t; Score 599.5;
t; Pred. No. 1.1e
41; Mismatches
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Pred. No. 1.0
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                                                                                                                                                       599.5; DB 2;
No. 1.1e-40;
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, 2000
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1.6e-43;
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                                                                    SEWINGGGTVQYT 60
                                                                                                     SWWSDGGAQATYT 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTMDÝQÍVÁVEGÝ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190;
YGWTTSPLVEYY 119
                                                                                                                                                                                                                                homology
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                                                                                                                                        3; Gaps
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RESULT 14
T50601
endo-1,4-beta-xylanase (EC 3.2.1.8) B, secreted [imported] -
N;Alternate names: xylanase B
C;Species: Streptomyces coelicolor
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_cha
C;Accession: T50601
R;Redenbach, M.; Kieser, H.M.; Denapaite, D.; Eichner, A.; C
Mol. Microbiol. 21, 77-96, 1996
A;Title: A set of ordered cosmids and a detailed genetic and
A;Reference number: Z20556; MUID:97000351; PMID:8843436
A;Accession: T50601
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-335 <RED>
A;Cross-references: UNIPROT:Q9RKN6; UNIPARC:UPI00000DC56E; E
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: xlnB
C;Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,
C;Keywords: glycosidase; hydrolase
A;Accession: PS0239
A;Molecule type: protein
A;Residues: 41-71 <SH2>
A;Cross-references: UNIPAL
C;Genetics:
A;Gene: xlnB
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JS0590
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                                                                                                                                                                    Gene 107, 75-82, 1991
A;Title: Sequences of three
A;Reference number: JS0589;
                                                                                                                                                                                                        endo-1,4-beta-xylanase (EC 3.2.1.8) B p N;Alternate names: xylanase B C;Species: Streptomyces lividans C;Date: 10-Mar-1994 #sequence_revision C;Accession: JS0590; PS0239 R;Shareck, F.; Roy, C.; Yaguchi, M.; McGene 107, 75-82, 1991
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                                                                                                    A;Accession: JS0590
A;Molecule type: DNA
A;Residues: 1-333 <SHA>
A;Cross-references: UNIPARC:UPI000017296A;
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Best Local S
Matches 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVA
                                                                                                                                                                                                                                                                                                                                                                                                    GTITTGNHFDAWARAGMPLGNFSYYMIMATEGYQSSGSSSINVGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                   GTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVADVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NMGSGGQYSTSWRNTGNFVAGKGWANG-GRRTVQYSGSFNPSGNAYLALYGWTSNPLVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVTLLVRSAWAVALAALALMLP---GTAQADTVVTTNQEGTNNGYYYSFWTDSQGTVSM
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larity 51.5%;
Conservative 2
                                     UNIPARC: UPI000017296B
                                                                                                                                                                       genes specifying xylanases in Streptomyees MUID:92077439; PMID:1743521
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Pred. No. 2.4e-39;
; Mismatches 73;
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                                                                                                                                                                                                                           Morosoli,
                                                                                                                                                                                                                                                                                                              precursor
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                                                                                                       GB:M64552
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                                                                                                                                                                                                                                                                                                                Streptomyces lividans
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                                                                                                                                                                                                                           Kluepfel,
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C; Function:
A; Description: catalyzes the hydrolysis of 1,4-beta-xylosidic A; Pathway: xylan degradation
C; Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-C; Keywords: extracellular protein; glycosidase; hydrolase; pol F; 1-40/Domain: signal sequence #status predicted <SIG>F; 41-333/Product: endo-1,4-beta-xylanase B #status experiments F; 54-230/Domain: endo-1,4-beta-xylanase homology <XYL>F; 127,217/Active site: Glu #status predicted
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Best Local Simi
Matches 112;
   196
                             188
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                                                                                                         ISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNP
                                                    DAWARAGLNVNGDHYYQIVATEGYFSSGYARITVADVG
                                                                                                                                                                 AWAVALARSPLMLP---GTAQADTVVTTNQEGTNNGYYYSFWTDSQG
                                                                                                                                                                                           ALAALAATGALAFPAGNATELEKROTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYE 67
Conservative
                                                                                                                                                                                                                                   46.3%;
51.4%;
                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                    Score 573; DB 1
Pred. No. 2.3e-3
4; Mismatches
                                                                                                                                                                                                                       38;
76;
                              225
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                                                        KRTSGTVQTGCHF 187
                                                                                                            LVBYYIVENFGTY 127
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Search completed: February 10, 2006, 15:02:20 Job time: 28.9236 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Q92245_MAGGR
O13447_COCCA
Q9GS1SA1_MAGGR
Q70T28_9PLEO
Q00350_COCCA
Q9HGE1_HUMGT
Q12579_9PEZI
XYN1_HUMIN
Q12580_9PEZI
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Q766V1_9ASCO
Q7SDQ1_NEUCR
Q02244_TRIRE
Q871E8_NEUCR
Q4MLV2_ASPFU
Q4MLV2_ASPFU
Q4MLV2_ASPFU
Q4MLV3_GHENI
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DT 10-MAY-2005 (Rel. 47, Last annotated)

DE Endo-1,4-beta-xylanase (EC 3.2.1.)

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MEDLINE=20090955; PubMed=10623548; DOI=10.1006/jmbi.1999.3348;
Kumar P.R., Eswaramoorthy S., Vithayathil P.J., Viswamitra M.A.;
"The tertiary structure at 1.59 A resolution and the proposed amino acid sequence of a family-11 xylanase from the thermophilic fungus
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tosporic Trichocomaceae; Paecilomyces
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J. Mol. Biol. 295:581-593(2000).
-!- CATALYTIC ACTIVITY: Endohydrolysis of linkages in xylans.
-!- BIOPHYSICOCHEMICAL PROPERTIES:
Temperature dependence:
Thermostable;
-!- PATHWAY: Xylan degradation.
-!- SIMILARITY: Belongs to the glycosyl h family.
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Interpro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PRINTS; PR00911; GLHYDRLASE11.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

3D-structure; Acetylation; Direct_protein se Hydrolase; Xylan degradation.

ACT_SITE 86 86 Nucleophile (By ACT_SITE 178 178 Proton donor (B MOD_RES 1 1 1 N-acetylglycine DISULFID 110 154

SEQUENCE 194 AA; 20947 MW; 1D5C50AA4F6ED
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Q1-MAY-2000
Q1-OCT-2003
XYlanase pred
Name=xyll;
NUCLEOTIDE SEQUENCE.

STRAIN=H2;

Degefu Y., Paulin L., Lubeck P.S.;

"Cloning, sequencing and expression of a x;

pathogen Helminthosporium turcicum Pass.";

Eur. J. Plant Pathol. 107:457-465(2001).

EMBL; AJ238895; CAB52417.1; -; Genomic_DNA
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Pleosporales; Pleosporaceae; (
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SMR; Q9UVZ3; 37-224.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-9
GO; GO:0005975; P:carbohydrate metabolism; IEA.

GO; GO:0045493; P:xylan catabolism; IEA.

InterPro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PRINTS; PR00911; GLHYDRLASE11.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

Signal; Xylan degradation.

Signal; Xylan degradation.

Potential.
                                                                       PARTIAL PROTEIN SEQUENCE:
Holden F.R., Walton J.D.;
Holden F.R., Walton J.D.;
"Xylanases from the fungal maize pathogen (
"Xylanases from the fungal maize pathogen (
Physiol. Mol. Plant Pathol. 40:39-47(1992)
-!- FUNCTION: Major xylan-degrading enzyme hydrolysis of arabinoxylan, the major
                                                                                                                                                                  NUCLEOTIDE SEQUENCE.

STRAIN=Race 1 / Isolate SB111;
STRAIN=Race 1 / Isolate SB111;
MEDLINE=94003417; PubMed=8400376;
Appel P.C., Panaccione D.G., Holden F.R., Walton J.D.;
"Cloning and targeted gene disruption of XYL1, a beta gene from the maize pathogen Cochliobolus carbonum.";
Mol. Plant Microbe Interact. 6:467-473(1993).
                                                                                                                                                                                                                                                                                                         XYN1 COCCA STANDARD; PRT; 221 AA. Q06562; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) Endo-1,4-beta-xylanase I precursor (EC 3.2.1.) beta-xylan xylanohydrolase 1). Name=XYL1;
              gene
Mol.
[2]
                                                                                                                                                                                                                                                                           Cochliobolus carbonum (Bipolaris zeicola).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Pleosporales; Pleosporaceae; Cochliobolus.
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walls.

CATALYTIC ACTIVITY: Endohydr linkages in xylans.

PATHWAY: Xylan degradation.

SUBCELLULAR LOCATION: Secret PTM: The N-terminus is block SIMILARITY: Belongs to the gfamily.
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MEDLINE=21654148; PubMed=11795847; DOI=10.1007/s00294-001-0:

MEDLINE=21654148; PubMed=11.0007/s00294-001-0:

MEDLINE=21654148; PubMed=11.0007/s00294-001-0:

MEDLINE=21654148; PubMed=11795847; DOI=10.1007/s00294-001-0:

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MEDLINE=21654148; PubMed=11.0007/s00294-001-0:

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MEDLINE=216541499; PubMed=116641499; PubMed=11664149949-001-0:

MEDLINE=21654149949494949494
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HSSP; O43097; 1YNA.
SMR; Q06562; 31-218.
InterPro; IPR001137; Glyco_hydro_11.
Pfam; PF00457; Glyco_hydro_11; 1.
PRINTS; PR00911; GLHYDRLASE11.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
Direct protein sequencing; Glycosidase; Hydrylan degradation.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariom;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
Fusarium oxysporum complex.
NCBI_TaxID=59765;
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Proton donor (By similarity).
W -> I (in Ref. 2).
G -> A (in Ref. 2).
S -> W (in Ref. 2).
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3 -> A (in Ref. 2).
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                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.

Lubeck P.S., Paulin L., Degefu Y., Lubeck M., Collinge "Molecular cloning and DNA sequencing of a xylanase ger phytopathogenic fungus Ascochyta pisi Lib.";

Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases EMBL; Z68891; CAA93120.1; -; Genomic_DNA.

RSP; O43097; 1YNA.

RMR; Q00263; 39-224.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-gly GO; GO:005975; P:carbohydrate metabolism; IEA.

GO; GO:0045493; P:xylan catabolism; IEA.

InterPro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11.

PROSITE; PR00911; GLHYDRLASE11.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.

SIGNAL 1 19 Potential.
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Q00263;
Q00263;
Q1-NOV-1996 (TrEMBLrel. 01, Create
01-NOV-1996 (TrEMBLrel. 01, Last s
01-OCT-2003 (TrEMBLrel. 25, Last a
Endo-1,4-betaxylanase precursor.
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Pfam; PF00457; Glyco_hydro_11; 1.

PRINTS; PR00911; GLHYDRLASE11.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1;

PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2;

Xylan_degradation.
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SEQUENCE
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
mitosporic Pezizomycotina; Ascochyta.
NCBI_TaxID=47971;
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148; Conservative
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ATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPL
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Pred. No. 8.4e
30; Mismatches
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Pred. No. 3.9e-57;
5; Mismatches 46
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annotation update)
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8.4e-58;
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RESULT

OCCUPANT

OCCUPANT
RESULT 8
013447 COCSA
ID 013447 COCSA
AC 013447;
DT 01-JAN-1
DT 01-JAN-1
DT 01-OCT-2
DE Beta-1,4
GN Name=xyl
OS Cochliob
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Wu S.-C., Darvill A.G., Albersheim P.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ database EMBL; AY144349; AAB06573.2; -; Genomic_DNA.

EMBL; AY144349; AAB06573.2; -; Genomic_DNA.

HSSP; O43097; IYNA.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-(GO; GO:0005975; P:carbohydrate metabolism; IEA.

GO; GO:0045493; P:xylan catabolism; IEA.

GO; GO:0045493; P:xylan catabolism; IEA.

InterPro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PROSITE; PR00911; GLHYDRLASE11.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.

Xylan degradation.
                                                             013447 COCSA
013447;
01-JAN-1998
01-JAN-1998
01-OCT-2003
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Q92245 MAGGR
Q92245;
01-FEB-1997
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Pred. No. 3.9e-53;
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cotina; Sordariomy
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Name=xyl2

Cochliobolus

sativus

(Bipolaris

sorokiniana)

sequence up annotation

update)

update)

Beta-1,4-xylanase

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RESULT 9
Q518A1 MAGGR
ID Q518A1,
AC Q518A1,
AC Q518A1,
DT 13-SEP-2
DT 13-SEP-2
DT 13-SEP-2
DT 13-SEP-2
DT 13-SEP-2
CO REMARYOTHER
GN MAGNAPOR
OC EUKARYOT
OC SORTAIN=7
RN [1]
RP NUCLEOTI
RC STRAIN=7
RA Ait-zahr
RA Ait-zahr
RA Arachchi
RA Bayul T.
RA Bayul T.
RA Bayul T.
RA Borowsky
RA Calvo S.
RA Fitzgera
RA Barickson
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RA Hagopian
RA Hagopian
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A Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
A Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
A Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
A Arachchi H., Armbruster J., Bachantsang P., Boguslavskiy L.,
A Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
A Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
A Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
A David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
A Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
A Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
A Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
A Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
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Best Local S
Matches 135
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Mycol. Res. 105:352-359(2001).

REMBL; AJ004802; CAA06151.1; -; Genomic_DNA.

REMBL; AJ004802; CHA06151.1; -; GO; GO:004553; F:hydrolase activity, hydrolyzing O-quadrate metabolism; IEA.

REMBL; AJ004802; CHA06151 IEA.

REMBL; AJ004802; F:hydrolase activity, hydrolism; O-quadrate metabolism; IEA.

REMBL; AJ004802; F:hydrolase activity, hydrolism; IEA.

REMBL; AJ004802; CHA06151.1; I.

REMBL; AJ004802; CHA06151.1; I.

REMBL; AJ004802; CHA06151.1; I.

REMBL; AJ004802; CAA06151.1; I.

REMBL; AJ004802; CAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q51SA1 MAGGR PRELIMINARY;
Q51SA1,
Q51SA1,
13-SEP-2005 (TrEMBLrel. 3
13-SEP-2005 (TrEMBLrel. 3
13-SEP-2005 (TrEMBLrel. 3
13-SEP-2005 (TrEMBLrel. 3
Hypothetical protein.
ORFNames=MG08424.4;
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Eukaryota; Fungi; Ascomycota; Posordariomycetes incertae sedis;
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Pleosporales; Pleosporaceae; Cochliobolus.
NCBI_TaxID=45130;
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                                                                                                                                                                                                                                                                                                                                                                       STRAIN-70-15;
                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=242507;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172
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58.7%;
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Last sequence update)
Last annotation update)
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Pred. No. 3.6e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pezizomycotina; Sordariomycetes; 
; Magnaporthaceae; Magnaporthe.
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                                                          Hafez N.,
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RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,

RA Lindblad-toh K., Liu X., Lokyitsang Y., Lucien O.,

RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,

RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,

RA McCarthy M., Mcdonough S., Mcghee T., Meldrim J., Meneus L.,

RA Mozes J., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C.,

RA Mozes J., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C.,

RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,

RA O'neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piqani B.,

Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,

RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,

RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,

RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,

RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Tohuinga P.,

RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,

Venkateraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,

RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,

The genome sequence of Magnaporthe grisea.";

Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                          preliminary data.

EMBL; AACU01001255; EAA49509.1; -; Genomic_
InterPro; IPR002453; Beta_tubulin.
InterPro; IPR001137; Glyco_hydro_11.
Pfam; PF00457; Glyco_hydro_11; 1.
PRINTS; PR00911; GLHYDRLASE11.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOW HYPOthetical protein.
SEQUENCE 204 AA; 22624 MW; 2396D83ED2B9
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STRAIN=70-15;
Dean R., Mitchell T.,
Submitted (OCT-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhu H., Blackmon B.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
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Kells
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STRAIN=70-15;
188
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                                                          QVAQSTRTNQPSIDGTRTFQQYWSVRQQKRSSGTVDMKKHFDA
                                                                                                                                                                                                                                                    Conservative
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to the
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65.1%;
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                                                                                                                                                                                                                                                               Score 711; DB 2;
Pred. No. 9.2e-52;
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                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic_DNA.
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W databases.
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Labutti K.,
wis T.,
Lucien O.,
                                                          3MKL-GTHDYQIV 187
                                                                                                                                                    IDLGTVECDGSIY 146
                                                                                                                                                                                                   GNLVGGKGWNPGL 86
                                                                                         3LNVNGDHYYQIV 206
                                                                                                                         SRKGTINVDGATY 128
                                                                                                                                                                                     NLVGGKGWNPG- 68
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RESULT
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DT Q00350
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Best Loc
Matches
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Biochimie 86:83-90 (2004).
EMBL; AJ548879; CAD70174.1; -; Genomic_DNA.
HSSP; P09850; 1BCX.
GO; GO:0004553; F:hydrolase activity, hydroly GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0045493; P:xylan catabolism; IEA.
InterPro; IPR001137; Glyco_hydro_11.
Pfam; PF00457; Glyco_hydro_11; 1.
PRINTS; PR00911; GLHYDRLASE11.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.
Signal; Xylan degradation.
SIGNAL 1 19 Potential.
                                                                                                                                                                                 QOO350 COCCA PRELIMINARY;
QOO350;
QOO350;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-OCT-2003 (TrEMBLrel. 2
Xyl2 precursor.
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Q70T28;
Q5-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xylanase precursor.
Name=xyl2;
Setosphaeria turcica.
Eukaryota; Fungi; Ascomycota;
Pleosporales; Pleosporaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
SEQUENCE
  STRAIN=SB111;
MEDLINE=97055717;
Apel-Birkhold P.C.
                                                                                             Cochliobolus carbonum (Bipolaris zeicola).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Pleosporales; Pleosporaceae; Cochliobolus.
NCBI_TaxID=5017;
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                                                                                                                                                                            Name=XYL2;
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33; Conservative
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231 AA;
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Pred. No. 1.2e-51;
0; Mismatches 56;
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Setosphaeria.
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RESULT 12
Q9HGE1 HUMGT E
AC Q9HGE1;
DT 01-MAR-2001 (7)
DT 01-OCT-2003 (7)
DE Beta-1,4-xylar
GN Name=xyn2;
OS Humicola grise
OC Eukaryota; Fur
OX NCBI_TaxID=55;
RN [1]
RP NUCLEOTIDE SEC
RC STRAIN=60849;
RA Faria F.P., PC
RL Submitted (JUD
DR EMBL; AF15559;
DR GO; GO:00454;
DR GO; GO:00457;
DR GO; GO:00457;
DR GO; GO:00457;
DR GO; GO:00457;
DR FROSITE; PS00;
DR PROSITE; PS00;
DR SGUENCE 22;
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                        Query Match
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Matches 128
                                                                      Faria F.P., Pocas-Fonseca M.J., Azevedo M.O.; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ EMBL; AF155594; AAG16891.1; -; Genomic_DNA. HSSP; O43097; 1YNA.

GO; GO:0004553; F:hydrolase activity, hydroly GO; GO:0005975; P:carbohydrate metabolism; IEGO; GO:0045493; P:xylan catabolism; IEA. InterPro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PRONITE; PR00911; GLHYDRLASE11.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

Xylan degradation.

SEQUENCE 227 AA; 25615 MW; 991815AD84EB29
                                                                                                                                                                                                                                                                                           Humicola grisea va
Bukaryota; Fungi;
NCBI_TaxID=5528;
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01-MAR-2001 (TrEMBL
01-OCT-2003 (TrEMBL
Beta-1,4-xylanase.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0004553; F:hydrolase activity, hydrolyzing GO; GO:0004553; F:carbohydrate metabolism; IEA.

InterPro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PRINTS; PR00911; GLHYDRLASE11.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
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                      Score 692.5;
Pred. No. 3.7e
19; Mismatches
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Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; D49850; BAA08649.1; -; Genomic_DNA.
PIR; S71472; S71472.
R HSSP; P36217; 1XYO.
R GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.
R GO; GO:0015975; P:carbohydrate metabolism; IEA.
R GO; GO:0045493; P:xylan catabolism; IEA.
R GO; GO:0045493; P:xylan catabolism; IEA.
R InterPro; IPR001137; Glyco_hydro_11.
R PF10457; Glyco_hydro_11; 1.
R PF10776; GLYCOSYL_HYDROL_F11_1; 1.
R PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.
R PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
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579 9PEZI
Q12579 9PEZI PRELIMINARY;
Q12579;
Q1-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-MAR-2004 (TrEMBLrel. 2
Endo-betal, 4-xylanase A (
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NUCLEOTIDE SEQUENCE.
MEDLINE=96118924; PubMed=8595661; DOI=10.1007/BF00313196;
Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.
"Two family G xylanase genes from Chaetomium gracile and expression in Aspergillus nidulans.";
Curr. Genet. 29:73-80(1995).
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Eukaryota; Fungi; Ascomycota; Po
Sordariomycetidae; Sordariales;
NCBI_TaxID=47794;
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                                                                                                              YTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVE
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3.2.1.8).
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Pred. No. 4.3e-50;
9; Mismatches 54;
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P55334; Q12625;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence updat
10-MAY-2005 (Rel. 47, Last annotation upd
Endo-1,4-beta-xylanase 1 precursor (EC 3.
beta-D-xylan xylanohydrolase 1).
                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                      genes.
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MEDLINE=94247364; PubMed=8190078;
Dalboege H., Hansen H.P.H.;
"A novel method for efficient exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humicola insolens.
Eukaryota; Fungi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      aryota; Fungi;
[_TaxID=34413;
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RESULT 15 Q12580 9PEZI ID Q12580_9PEZI I

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C 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
T 01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
T 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E Endo-betal, 4-xylanase (EC 3.2.1.8).

Name=cgx8;
Chaetomium gracile.
SC Chaetomium gracile.
Cukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.

X NCBI_TaxID=47794;
N [1]
NUCLEOTIDE SEQUENCE.
MEDLINE=96118924; PubMed=8595661; DOI=10.1007/BF00313196;
Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
"Two family G xylanase genes from Chaetomium gracile and their expression in Aspergillus nidulans.";
Curr. Genet. 29:73-80(1995).

N NICLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsukagoshi N.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; D49851; BAA08650.1; -; Genomic_DNA.

RIR; S71473; S71473.

RISSP; Q8J1V6; 1H1A.

RSSP; Q8J1V6; 31-220.

RO; G0:0031176; F:endo-1,4-beta-xylanase activity; IEA.

GO; G0:0031176; F:carbohydrate metabolism; IEA.

InterPro; IPR001137; Glyco_hydro_11.

Refam; PF00457; Glyco_hydro_11; 1.

RRINTS; PR00911; GLHYDRLASE11.

RROSITE; PS00776; GLYCOSYL HYDROL_F11_1; 1.

Glycosidase; Hydrolase; Xylan degradation.

Glycosidase; Hydrolase; Xylan degradation.

SEQUENCE 241 AA; 25564 MW; DCD4B012272F777F CRC64;
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Tsukagoshi N.;
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Similarity 59.5%;
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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| | / Match Local 1es 22 | IELEFAX TELEFAX INFORMATION SEQUENCE (LENGTH: TYPE: TYPE: TOPOLOG) MOLECULE 1 08-886-765-2 | CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Lambiris, Elias J REGISTRATION NUMBER: 33,728 REFERENCE/DOCKET NUMBER: 4324 TELECOMMUNICATION INFORMATION: | COMPUTER READABLE FORM: COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatib OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for CURRENT APPLICATION DATA: APPLICATION NUMBER: US FILING DATE: 1-JUL-199 | ADDRESSEE: 1 STREET: 405 CITY: New York STATE: NY COUNTRY: US | APPLICANT: Hansen, APPLICANT: Wagner, APPLICANT: Wallertz APPLICANT: Mullertz APPLICANT: Knap, In TITLE OF INVENTION: NUMBER OF SEQUENCES: | ESULT 1 S-08-886-7 Sequence Patent No | ហ្ | ហុហ្គូស្គូ | <u> </u> | |
| ч | 22 1 25 | TELEPHONE: 212-86/-0123 TELEPAX: 212-878-9655 RMATION FOR SEQ ID NO: QUENCE CHARACTERISTICS: LENGTH: 225 amino acids TYPE: amino acid TOPOLOGY: linear LECULE TYPE: protein 86-765-2 | SIF STR STR MMU | MPUTER READABLE FORM: MPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ for Wi- RRENT APPLICATION DATA: APPLICATION NUMBER: US/0 FILING DATE: 1-JUL-1997 | ADDRESSES: ADDRESSES: STREET: 4 CITY: New STATE: NY COUNTRY: | ANT ANT OF OF | | 55 55 55 55 55 55 55 55 55 55 55 55 55 | 568 568 568 | 630.5 630.5 628 610.5 588.5 588.5 | |
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| TPVI | larity Conser | 12-878 SEQ I ACTERI 5 amin o acid linear | TION IN | ABLI IBM IBM YSTI Fast CATI | | ATION: Hansen, Wagner, Mullert Knap, I ENTION: QUENCES | icat | | 556777 | 77.53.30.9 | |
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| LAAI | 100. 100. tive | 212-878-9655 212-878-9655 FOR SEQ ID NO: HARACTERISTICS: 225 amino acid mino acid mino acid ininear ': linear ': linear | 35 MATI Liae R: UMBE FORM | JE FORM: Diskette Compatil Compatil Compatil Compatil Compatil LOS LEM: DOS | 5817500o ington A | Peter Peter Trz, Ane Inge He Anima | us/ | 344 | 296 335 335 231 215 189 | 190 1225 225 223 226 296 296 | |
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NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local S
Matches 225
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APPLICANT:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM
MEDIUM TYPB: Disket
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ADDRESSEE: No. 6245
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                TYPE: amino acids
TOPOLOGY: lin-
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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CITY: New York
STATE: NY
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               VENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT
                                                           LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI
                                                                            LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI
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 VENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT
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Mullertz, Anette
Knap, Inge Helmer
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larity 100.0%; Pred. No. 7.9e-110;
Conservative 0; Mismatches 0;
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Patent No.
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APPLICANT: Dahiyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
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                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
SEQ ID NO 23
-09-570-856B-23
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NAME/KEY: MISC_FEATU
LOCATION: (1)...(1)
OTHER INFORMATION: "
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            ORGANISM: Paecilomyces variotii
                                     LENGTH: 194
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TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH 61
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                                                                 version 3.1
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Pred. No. 3.6e-95;
0; Mismatches 0;
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RESULT 6
US-08-458-023B-4
; Sequence 4, Application US; Sequent No. 5667990
; Patent No. 5667990
; GENERAL INFORMATION:
APPLICANT: Berka, Rance APPLICANT: Yoder, Wence APPLICANT: Takagi, Shi APPLICANT: Boominathar APPLICANT: AVENTION: AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-09-570-856B-29
; Sequence 29, Application US/09570856B
; Patent No. 6682923
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, ORGANISM: Cochliobolus
US-09-570-856B-29
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APPLICANT: Bentzien, Joerg M
APPLICANT: Dahiyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
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Best Local S
Matches 169
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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T: Berka, Randy M.
T: Yoder, Wendy
T: Takagi, Shinobu
T: Boominathan, Karuppan C.
INVENTION: ASPERGILLUS EXPRESSION
                                                                                                                                                                                                                                                                                                       GAGGSYSVSWGSGGNLVGGKGWNPG-TARTITYSGTYNYNGNSYLAVYGWTRNPLVEYYV
                                                                                                                                                                                                                                                                                                                          LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI
                                                                                                                                                                                                                                                                                                                                                                                      MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATYTN
                                                                                                                                                                                                                                                                                                                                                                VENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT
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                                                                                                                                                                                 VNMKTHFDAWASKGMNL-GQHYYQIVATEGYFSTGNAQITV
                                                                                                                                                                                                                                            VENFGTYDPSSQSQNKGTVTSDGSSYKIAQSTRTNQPSIDGTRTFQQYWSVRQNKRSSGS
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llarity 87.6%;
Conservative 1
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Pred. No. 8.4e-69;
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Pred. No. 6e-84;
l; Mismatches
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  SYSTEM
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GENERAL INFORMATION:

APPLICANT: WATANABE, MANABU

APPLICANT: MORIYA, TATSUKI

APPLICANT: MORIYA, KAORU

APPLICANT: SUMIDA, NAOMI

APPLICANT: MURAKAMI, TAKESHI

TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE cbl

TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR

TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH

FILE REFERENCE: 99-0266*/LC(WMC)/00144

CURRENT APPLICATION NUMBER: US/09/254,733

CURRENT FILING DATE: 1999-05-07

NUMBER OF SEQ ID NOS: 52
                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-09-254-733-7
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REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
SOFTWARE: PatentIn Ver.
SEQ ID NO 7
LENGTH: 223
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                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LOWER BOOK AND ADDRESS FILE AND ADDRESS FILE AND ADDRESS FILE ATTORNEY/AGENT INFORMATION:
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ZIP: 10174-6201
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5. 6277596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQYTNLEGSRYQVRWRNTGNFVGGKGWNPG-TGRTINYGGYFNPQGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MVGFTPVALAALAATGALA-----FPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEYYVIESYGTYNÞGSQAQYKGTFYTDGDQYDIFVSTRYNQÞSIDGT
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, Karen A.
BER: 31,274
BER: 4086.010-US
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; TYPE: PRT
; ORGANISM: TRICHODERMA VIRIDE MC300-1
US-09-254-733-7
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Best Local 8
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APPLICATION NUMBER: US 07/524,308
FILING DATE: 16-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.008000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gullandelmo, Marja
APPLICANT: Paloheimo, Marja
APPLICANT: Lahtinen, Tarja
APPLICANT: Fagerstr m, Richard
TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods
TITLE OF INVENTION: for Their Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/01 FILING DATE: 16-SEP-1993 PRIOR APPLICATION DATA:
                                                                                                                           APPLICATION NUMBER: US 07/889,893
FILING DATE: 29-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/078,478 FILING DATE: 18-JUN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                          APPLICATION NUMBER: PCT/FI93/00221
FILING DATE: 24-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVGFTPVALAALAATGALAFPAG--NATELEKROTTPNSEGWHDGYYYSWWSDGGAQATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNGPGGQFSVNWSNSGNFVGGKGWQPGTKNKVINFSGTYNPNGNSYLSVYGWSRNPLIEY 120
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1100 New York Avenue,
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Saarelainen, Ritva
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Pred. No. 2.7e-57;
2; Mismatches 62;
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; MOLECULE TYPE: protein US-08-121-436A-2
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US-08-768-373-2
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Best Local Similarity
Matches 128; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
                                                                                                                                                                                          ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEI STREET: 1100 NEW YORK AVENUE, SUITE CITY: WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                 APPLICATION NUMBER: US/08/768,373 FILING DATE: 17-DEC-1996
                                                                                                                                                                                                                                                                                                            STATE:
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LANTTO, RAIJA
LAHTINEN, TARJA
FAGERSTR M, RICHARD
SUOMINEN, PIRKKO
NVENTION: NOVEL XYLAN
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M NTYL , ARJ
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Pred. No. 3.4e
32; Mismatches
                                                                                                                                                                                                              Version
                                                                                                                                                                                                                                                                                                                                                                                                           GENES
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3.4e-57;
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60/008,746

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NAME/KEY: Protein
LOCATION: 1.261
OTHER INFORMATION:
US-08-768-373-2
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US-09-849-242A-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application Patent No. 6635464
GENERAL INFORMATION:
APPLICANT: PALO
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Best Local Similarity
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                                                     ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION NUMBER: US/09/849,242A
APPLICATION NUMBER: US/09/849,242A
PILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEI
STREET: 1100 NEW YORK AVENUE, SUITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LESGGQYSVTWSGNGNWVGGKGWNPGTDNRVINYTADYRPNGNSYLAVYGWTRNPLIEYY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MVNFSTLFLAASTAALAAAAAPS-----IEKRQTLTSSATGTHNGYYYSFWTDGQGNIRFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: WASHINGTON STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSG 179
APPLICATION DATA:
APPLICATION NUMBER: US 08/768,373
FILING DATE: 17-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUOMINEN, PIRKY
INVENTION: NOVEL
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LAHTINEN, TARJA
FAGERSTRTM, RICHARD
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LANTTO, RAIJA
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MONTYLO, ARJ
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                                                                                                                                                                                                                                                Version
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NAME/KEY: Protein
; LOCATION: 1..261
; OTHER INFORMATION: /1
; SEQUENCE DESCRIPTION: SEQ
US-09-849-242A-2
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US-08-044-621D-29
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                                                                                                                                                                                                                                                                          Sequence 29, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Wakarchuk
APPLICANT: Wing L. Sung
APPLICANT: Makoto Yaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 371-2:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                            COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                       TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANT.
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
                                                                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60
FILING DATE: 18-DEC-1995
APPLICATION NUMBER: US 60
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION
ATTORNEY/AGENT ATTORNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 1716.0540004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
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                                                                                                                     Ottawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVNFSTLFLAASTAALAAAAPS-----IEKROTLTSSATGTHNGYYYSFWTDGOGNIRFN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVESFGTYDPSTGATRMGSVTTDGGTYNIYRTQRVNAPSIEGTKTFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CIMBALA, MICHELE A. REGISTRATION NUMBER: 33,851
                                                                                                   Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITV 221
                                                                                                                                 EE: Gowling,
Suite 2600,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVTMANHFNAWROAGLQL-GSHDYQIVATEGYYSSGSATVNV
                                                                                                                                                                                                                                        Wing L. Sung
Makoto Yaguchi
Robert L. Campb
David R. Rose
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                                Diskette,
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 PC-DOS
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160 Elgin Street
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                                  5.25
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3Q ID NO: 2:
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Pred. No. 1.6e-56;
l; Mismatches 56;
                                in.,
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                                  360kB storage
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; PAGES: Abstract 676
; DATE: 1988
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN S
US-08-044-621D-29
RESULT 12
US-08-709-912-9
; Sequence 9, Application US/08709912
; Patent No. 5759840
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Best Local Similarity 61.3
Conservative
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US
FILING DATE: April 8,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Schizophyllum commune
STRAIN: Schizophyllum commune, I
IMMEDIATE SOURCE:
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
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PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
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TYPE: A
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REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
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                                                                      183
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                                                                                                                                         RVNAPSIDGTQTFDQYWSVRQDKRT-----SGTVQTGCHFDAWARAGLNVNGDHYYQIVA 207
                                                                                             TEGYFSSGYARITV
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No
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ER: 08-863796
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t; Pred. No. 3.2e-55;
26; Mismatches 43;
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PUBLICATION INFORMATION:
AUTHORS: Oku, T
AUTHORS: Yaguchi, M
AUTHORS: Parse, M
AUTHORS: Jurasek, L
JOURNAL: Canadian Fed.
PAGES: Abstract #676
DATE: 1988
US-08-709-912-9
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ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
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Best Local S
Matches 119
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APPLICANT: Sung D
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 277 Par
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
183
                                                                   123
                                                                                                   153
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119; Conservative
                                                                                                                                     63
                                                                                                                                                                                                                   34 TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGWNPGLNARAIH 92
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                                                                                                                                 FEGVYQPNGNSYLAVYGWTRNSLIEYYIVESYGSYDPSSGATDLGTV

SGTYQPNGNSYLAVYGWTRSSLIEYYIVESYGSYDPSSGATDLGTV
                                                                                                                                                                                              TPSSTGTDGGYYYSWWTDGAGDATYQNNGGGSYTLTWSGNNGNLVGGKGWNPGAASRSIS 62
                                                                RYNAPSIDGTQTFEQFWSVRNPKKAPGGSISGTVDVQCHFDAWKGLGMNLGSEHNYQIVA 182
                                                                                   RVNAPSIDGTQTFDQYWSVRQDKRT----
 TEGYOSSGTATITY
                              TEGYFSSGYARITY 221
                                                                                                                                                                                                                                                                                                                                                                         : Jurasek, L: Canadian Fed. Biol. Soc.Abstract #676
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277 Park Ave.
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Yaguchi Dr., Makoto
Ishikawa Dr., Kazuhiko
VENTION: Modification of Xylanase to Improve
VENTION: Thermophilicity, Alkalophilicity and
VENTION: Thermostability
EQUENCES: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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196
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                                                                                               SGTVQTGCHFDAWARAGLNVNGDHYYQIVA 207
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                                                                                                                                                                     ECDGSIYRLGKTT 152
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; JOURNAL: Car
; PAGES: Abst:
; DATE: 1988
US-09-047-370-9
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US-09-047-370-9
                                                                                                 Query Match
Best Local Similarity
Matches 119; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                            PUBLICATION INFORMATION:
AUTHORS: Oku, T
AUTHORS: Yaguchi, M
AUTHORS: Parse, M
AUTHORS: Jurasek, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ISHIKAWA Dr. TITLE OF INVENTION: Mod TITLE OF INVENTION: The TITLE OF INVENTION: The NUMBER OF SEQUENCES: 54 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 00
APPLICATION NUMBER: US 00
FILING DATE: 09-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                   STRAIN:
                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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40. 5866408
34
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                                                                                                                                                                                 S: Yaguchi, M
S: Parse, M
S: Jurasek, L
L: Canadian Fed.
Abstract #676
                                        TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGWNPGLNARAIH
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§: Pitzpatric,
277 Park Ave.

                                                                                                53.6%;
Conservative 26
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Yaguchi Dr., Makoto
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                                                                                                                                                                                                                                                                                                                                                                     protein
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                                                                                               score 663; DB 1; Pred. No. 3.2e-55; Pred. No. 3.2e-55; Mismatches 43
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US-09-570-856B-18
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Patent No.
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SOFTWARE: PatentIn version
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bentzien, Joerg M
APPLICANT: Dahiyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
                                                                                                                                                                                                        GENERAL
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                                                                                            APPLICANT:
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                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                       CORRESPONDENCE ADDRESS:
                                                                                                                         APPLICANT:
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                        ADDRESSEE:
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1100 NEW WASHINGTON
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                                                  LANTILE,
LAHTINEN, TARUM
FAGERSTR M, RICHARD
SUOMINEN, PIRKKO
INVENTION: NOVEL XYLAN
INVENTION: AND USES TH
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LANTTO, RAIJA
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           STERNE, KESSLER, G
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Pred. No. 3.2e-55;
           GOLDSTEIN & SUITE 600
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                                                                                  GENES
                           FOX,
                                                                                  ENCODING
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: protein
ORGANISM: Chaetomium thermophilum
STRAIN: CB3730.95
FEATURE:
NAME/KEY: Protein
LOCATION: 1.230
OTHER INFORMATION: /label= XLNB
US-08-768-373-4

53.5%; Score 662.5
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Search completed: February Job time: 39.1265 secs
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COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                          188
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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   1238
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1088
821.5
802.5
794.5
7789.5
7716.5
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1238
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    Query
Match
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714.573 Million cell updates/s
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1: /cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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      GenCore (c) 1993
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US-09-467-368-2
US-10-237-386-24
US-10-237-386-21
US-10-237-386-21
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US-10-237-386-20
US-10-425-115-267585
US-10-237-386-25
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   Sequence
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 2, Appli
20, Appl
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27, Appl
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US-09-467-368-2
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ALIGNMENTS

APPLICANT: Hansen, Peter Kan Wagner, Peter Mullertz, Anette

Kamp

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US-09-467-368-2
                                                                                                                                                                   COUNTRY: USA
ZIP: 10174
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.C
RENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,368
FILING DATE: 21-Dec-1999
CLASSIFICATION ET : CURROWN>
PRIOR APPLICATION UMBER: US/08/886,765
FILING DATE: 1-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324.204-US
TELEPHONE: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acids
Query Match
Best Local Similarity
Matches 225; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US20020160080Alo No. US2002016008
STREET: 405 Lexington Avenue
CITY: New York
                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NY
   100.0%; Score 1238; llarity 100.0%; Pred. No. 1. Conservative 0; Mismatches
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No
                        .6e-109;
                                           DB 3;
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; ORGANISM: T.
US-10-237-386-24
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APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
ITITLE OF INVENTION: Xylanse Variants Having Al-
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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US-10-307-441-20
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SEQ ID NO 24
LENGTH: 225
Sequence 20, Application US/10307441
Publication No. US20030166236A1
GENERAL INFORMATION:
APPLICANT: SUNG, Wing L.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Modified Xylanases Exhibitin
TITLE OF INVENTION: and Alkalophilicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/10237386 Publication No. US20030180895A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1238; DB 4; Best Local Similarity 100.0%; Pred. No. 1.6e-109; Matches 225; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                             LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHPEGVYQPNGNSYLAVYGWTRNPLVEYYI 120
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                       Exhibiting
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Publication No. US20050214410A1;
GENERAL INFORMATION:
APPLICANT: Iogen Bio-Products Corporation
APPLICANT: White, Theresa C
APPLICANT: White, Theresa C
APPLICANT: Wallace, Katie E.A.;
TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expricant Application NUMBER: US/11/088,725A;
CURRENT APPLICATION NUMBER: US/11/088,725A;
CURRENT FILING DATE: 2005-03-25;
PRIOR APPLICATION NUMBER: US 60/556,061
PRIOR FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.2
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; TYPE: PRT
; ORGANISM: Thermomyces
US-10-307-441-20
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; TYPE: PRT
; ORGANISM: Thermomyces
US-11-088-725A-46
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US-11-088-725A-46
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; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
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Best Local Similarity
Matches 194; Conser
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Best Local
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                                                                                                                                                                                                                                       Similarity
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                                                             TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVN(
TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 211
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                                                                                                                                                                                                                   87.9%; Score 1088; DB 6; llarity 100.0%; Pred. No. 2.5e-95; Conservative 0; Mismatches 0;
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Pred. No. 2.5e-95;
0; Mismatches 0;
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; ORGANISM: H.
US-10-237-386-21
       APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
ITITLE OF INVENTION: Xylanse Variants Having Al
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR PILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
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APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                    Sequence 20, Application US/10237386 Publication No. US20030180895A1 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Sibbesen, (
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                                                                                                                                                                                                                                                                                                                                                                                                                                         VEYYIVENFGTYDPSSGATDLGTVBCDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATYTNGAGGSYSVSWGTGGNLVGGKGWNPG-TARTITYSGQYNPNGNSYLAIYGWTRNPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVSFTSITAAVAATGALAAPATDIAARAPSDLVARQSTPNGEGTHNGCFYSWWSDGGAR
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Conservative 25;
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Pred. No. 7.3e
25; Mismatches
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hes 41;
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US-10-425-115-221836
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RESULT
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SEQ ID NO 20
LENGTH: 221
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SEQ ID NO 221836
LENGTH: 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Ac
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/11
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                                                                                                 ATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPL 115
                                                                                                                                                                                                                                                                     MVGFTPVALAALAATGALAFPAGNAT----ELEKRQTTPNSEGWHDGYYYSWWSDGGAQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQATYTN 60
                                                                            RTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITV
                                                                                                                                                 VEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGT
                                                                                                                                                                                   TYTNGAGGSYSVNWGSGGNFVGGKGWNPG-SARTVTYSGSYNPNGNSYLAIYGWTRNPL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhou, III.
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                                                  RSSGSVNMKTHFDAWASKGMTL-GSHYYQIVATEGYFSTGSASITV
                                                                                                                  VEYYVVENFGTYDPSSQASNKGTVTADGSSYKIAQSTRTNQPSIDGT
                                                                                                                                                                                                                                                     MVSFTSLITAAVAATGAFAAPATDVAARSSGDLVARQSTPNAEGTHNGCFYSWWTDGGSK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MVSFTSIITAAVAATGALAAPATDVS-LVARQNTPNGEGTHNGCFWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VENFGTYDPSSQSQNKGTVTSDGSSYKIAQSTRTNQPSIDGTRTFQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kovalic, Da
Zhou, Yihua
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       Clone ID: MRT4577_133906C.1.pep
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67.9%; Pre
ative 26;
                                                                                                                                                                                                                                                                                                                                     64.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/10/425,115
                                                                                                                                                                                                                                                                                                                Score 794.5; Db .,
Pred. No. 2.7e-67;
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Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
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                                                                                                                    RTFQQYWSVRQNK 179
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                                                                                                                                                  TFDQYWSVRQDK 175
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APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Alt
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 227
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 267585
LENGTH: 221
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; ORGANISM: A. US-10-237-386-22
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US-10-237-386-22
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Best Local
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NAME/KEY: unsure
LOCATION: (1)..(221)
OTHER INFORMATION: U
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                                 LENGTH: 22
TYPE: PRT
                                                                                                                                                                                                                                                                                                                      APPLICANT: Danisco A/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VENFGTYDPSSQSQNKGTVTSDGSSYKIAQSTRTNQPSIDGTRTFQQYWSVRQNKRSSGS
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Pred. No. 7.9e-67;
6; Mismatches 45;
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GENERAL INFORMATION:

APPLICANT: La ROSa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules a

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 361946

LENGTH: 234
                  RESULT 11
US-10-237-386-26
; Sequence 26, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
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Best Local S
Matches 148
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, (
APPLICANT: Sorensen, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 361946, Application US/10425115 Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            Matches
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ORGANISM: Zea mays
FEATURE:
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                                                                                                                                                                                                                                                                                                      RTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITV
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                                                                                                                                                              RODKRISGIVQIGCHFDAWARAGLNVNGDHYYQIVAIEGYFSSGYARIIV 221
                                                                                                                                                                                                          RNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPS:
                                                                                                                                                                                                                                                               GGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSSGSVNMKTHFDAWAAKGMKL-GTHNYQIVATEGYFSSGSAQITV
                                                                                                                                                                                      RNPLVEYYVVENFGTYDPSSAASVKGSVTADGSSYKIAQTQRVNQPSIDGTKTFNQYWSV 179
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                                                                                                                                        RONKRSSGSVNMKTHFDAWASKGMQL-GQHNYQIVA
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65.5%; Pred. No. 1.7;
live 25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                            27;
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                                                                                                                                                                                                              IDGTQTFDQYWSV 171
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APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Alt
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.0
SEQ ID NO 25
LENGTH: 231
TYPE: PRT
ORGANISM: C. carbonum
US-10-237-386-25
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; Sequence 25, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.0
                                                                       Query Match
Best Local S
Matches 132
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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor FILE REFERENCE: 674509-2046
                                                                         Local Sir
hes 132,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 58.7 tos 135; Conservative
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MVSFKSLLLAAVATTSVLAAPFDFLRERDDVNATALLEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGSAQYTMGEGSRYSVTWRNTGNFVGGKGWNPG-TGRVINYGGAFNPQGNGYLAVYGWT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.9%; Score 716.5; DB 4; 58.7%; Pred. No. 7.4e-60; 70. Miamatches 55;
                                                                                       56.7%;
                                                                   Score 701.5; DB 4;
Pred. No. 2e-58;
1; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Altered Sensitivity to Xylanase Inhibito
                                                                                                      Length
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                                                                                                        231;
                                                                     11;
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                                                                     Gaps
                                 51
60
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GENERAL INFORMATION:

APPLICANT: Danisco A/S

APPLICANT: Sibbesen, Ole

APPLICANT: Sorensen, Jens

TITLE OF INVENTION: Xylanse Variants Having

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/10/237,386

CURRENT FILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: PCT/IB01/00426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 219
; TYPE: PRT
; ORGANISM: C.
US-10-237-386-29
                                                                                                                                                         US-10-237-386-27; Sequence 27, Application US/10237386; Publication No. US20030180895A1
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US-10-237-386-29
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Best Local S
Matches 133
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Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
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APPLICANT: Sorensen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 000585.5
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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                                                                                                                                                                                                                                                                                                       SGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVA 222
                                                                                                                                                                                                                                                                                                                                          YYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTI
                                                                                                                                                                                                                                                                                                                                                                                                                YONGAGGSYSVOWONCGNFVGGKGWNPGA-ARTINFSGTFSPQGNGY
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Pred. No. 1.7e-57;
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FYSFWTDGGGTVN 56
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; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 227
; TYPE: PRT
; ORGANISM: H. insolens
US-10-237-386-27
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; TYPE: PRT
; ORGANISM: C:
US-10-237-386-35
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APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Alt
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35, Application US/10237386 Publication No. US20030180895A1 GENERAL INFORMATION:
                                                                                                                                                                                           Query Match 55.7%; Score 689; DB 4; Length 241; Best Local Similarity 59.5%; Pred. No. 3.3e-57; Matches 132; Conservative 31; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Danisco A/S
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                                                                                                                MVGFTPVALAALAATGALA-----FPAGNATELEKRQTTPNSEGWHDGYYYSWWSDGGAQ
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                                                                     NLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYY 119
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IVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSG 179
                                    NEAGGQYSVTWSGNGNWVGGKGWNPG-SARTINYTANYNPNGNSYLAVYGWTRNPLIEYY
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/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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| 26 563 45.5 239 7 US-11-170-653-40 Sequence 40, Appl 27 562.5 45.4 241 7 US-11-170-653-41 Sequence 41, Appl 260 45.2 193 7 US-11-108-163B-14 Sequence 41, Appl 260 45.2 217 7 US-11-108-163B-13 Sequence 14, Appl 27 US-11-108-163B-13 Sequence 14, Appl 27 US-11-108-163B-13 Sequence 14, Appl 28 Sequence 15, Appl 29 560 45.2 217 7 US-11-108-163B-12 Sequence 12, Appl 29 58.5 45.1 354 6 US-10-517-939-216 Sequence 11, Appl 35 551 44.5 358 6 US-10-517-939-18 Sequence 216, Appl 35 551 44.5 358 6 US-10-517-939-196 Sequence 196, Appl 36 541.5 43.7 347 6 US-10-517-939-196 Sequence 196, Appl 39 539.5 43.6 352 6 US-10-517-939-262 Sequence 262, Appl 39 539.5 43.6 352 6 US-10-517-939-262 Sequence 262, Appl 39 539.5 43.6 352 6 US-10-517-939-368 Sequence 262, Appl 31.5 42.9 303 6 US-10-517-939-316 Sequence 27, Appl 31.5 42.9 303 6 US-10-517-939-316 Sequence 27, Appl 31.5 42.9 303 6 US-10-517-939-316 Sequence 370, Appl 32.5 42.6 237 7 US-11-170-653-47 Sequence 214, Appl 32.7 542.6 346 6 US-10-517-939-234 Sequence 234, Appl 352.6 34.6 35.6 GUS-10-517-939-234 Sequence 234, Appl 352.4 42.3 356 6 US-10-517-939-234 Sequence 234, Appl 35 |
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| 45.5 239 7 US-11-170-653-40 Sequence 40, 45.4 241 7 US-11-170-653-43 Sequence 41, 45.3 242 7 US-11-108-163B-14 Sequence 41, 45.2 193 7 US-11-108-163B-13 Sequence 11, 45.2 217 7 US-11-108-163B-12 Sequence 12, 45.2 301 7 US-11-108-163B-11 Sequence 11, 45.1 354 6 US-10-517-939-216 Sequence 11, 45.1 358 6 US-10-517-939-182 Sequence 216, 44.7 240 7 US-11-170-653-38 Sequence 182, 43.7 347 6 US-10-517-939-196 Sequence 196, 43.7 216 7 US-11-170-653-45 Sequence 196, 43.7 216 7 US-11-170-653-45 Sequence 226, 43.7 242 6 US-10-517-939-262 Sequence 226, 43.0 445 6 US-10-517-939-268 Sequence 226, 42.9 303 6 US-10-517-939-214 Sequence 214, 42.9 358 6 US-10-517-939-214 Sequence 214, 42.6 237 7 US-11-170-653-47 Sequence 370, 42.6 346 6 US-10-517-939-234 Sequence 234, 42.3 356 6 US-10-517-939-234 Sequence 234, |
| Sequence 40, 13 242 7 US-11-170-653-40 Sequence 40, 241 7 US-11-170-653-43 Sequence 41, 2193 7 US-11-108-163B-14 Sequence 11, 2193 7 US-11-108-163B-13 Sequence 13, 22 217 7 US-11-108-163B-12 Sequence 13, 22 220 7 US-11-108-163B-11 Sequence 12, 2301 7 US-11-108-163B-11 Sequence 12, 240 7 US-11-170-653-38 Sequence 11, 254 6 US-10-517-939-216 Sequence 216, 27 240 7 US-11-170-653-45 Sequence 182, 27 240 7 US-11-170-653-45 Sequence 196, 27 216 7 US-10-517-939-262 Sequence 196, 27 246 Sequence 226, 28 Sequence 236, 29 303 6 US-10-517-939-214 Sequence 214, 29 358 6 US-10-517-939-370 Sequence 214, 29 358 6 US-10-517-939-234 Sequence 234, 356 6 US-10-517-939-234 Sequence 234, 356 6 US-10-517-939-234 Sequence 234, 356 Sequ |
| 7 US-11-170-653-40 Sequence 40, US-11-170-653-43 Sequence 41, Sequence 43, US-11-108-163B-14 Sequence 41, US-11-108-163B-13 Sequence 11, Sequence 12, US-11-108-163B-12 Sequence 12, US-11-108-163B-11 Sequence 12, US-11-108-163B-11 Sequence 12, US-11-170-653-38 Sequence 11, Sequence 12, US-11-170-653-45 Sequence 182, US-10-517-939-196 Sequence 196, US-10-517-939-262 Sequence 262, US-10-517-939-268 Sequence 276, US-10-517-939-276 Sequence 276, US-10-517-939-276 Sequence 276, US-10-517-939-270 Sequence 276, US-10-517-939-270 Sequence 277, US-10-517-939-234 Sequence 274, Sequence 274, US-10-517-939-234 Sequence 234, |
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| -11-170-653-40 Sequence 40, -11-170-653-43 Sequence 43, -11-170-653-41 Sequence 41, -11-108-163B-13 Sequence 11, -11-108-163B-13 Sequence 12, -11-108-163B-11 Sequence 12, -11-108-163B-11 Sequence 11, -10-517-939-182 Sequence 216, -11-170-653-45 Sequence 45, -10-517-939-262 Sequence 262, -10-517-939-368 Sequence 264, -10-517-939-368 Sequence 27, -10-517-939-370 Sequence 214, -10-517-939-160 Sequence 27, -10-517-939-160 Sequence 234, -10-517-939-234 Sequence 234, -10-517-939-234 Sequence 234, -10-517-939-234 |
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SOPTWARE: Pate: SEQ ID NO 24 LENGTH: 225 TYPE: PRT ORGANISM: T. US-11-170-653-24 APPLICANT: Danisco A/S APPLICANT: Sibbesen, Ole APPLICANT: Sibbesen, Jens TITLE OF INVENTION: Xylanse Variants Having Alt FILE REFERENCE: 674509-2046 CURRENT APPLICATION NUMBER: US/11/170,653 CURRENT FILING DATE: 2005-06-23 PRIOR APPLICATION NUMBER: US/10/237,386 PRIOR FILING DATE: 2002-09-09 PRIOR FILING DATE: 2001-03-08 PRIOR APPLICATION NUMBER: PCT/IB01/00426 PRIOR FILING DATE: 2001-03-08 PRIOR FILING DATE: 2000-03-08 PRIOR FILING DATE: 2000-03-08 PRIOR APPLICATION NUMBER: GB 0015751.1 PRIOR APPLICATION NUMBER: GB 0015751.1 PRIOR FILING DATE: 2000-06-27 NUMBER OF SEQ ID NOS: 66 PatentIn version lanuginosus Altered Sensit ivity to Xylanase Inhibitor:

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LEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAV)

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VENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQY

IYRLGKTTRVNAPSIDGTQTFDQ

WSVRQDKRTSGT 180

GWTRNPLVEYYI 120

VQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVADVG

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25 25

VQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVADVG

MVGFTPVALAALAATGALAFPAGNATELEKRQTTPNSEGWHDGYYYS

SWWSDGGAQATYTN 60

Query Match
Best Local Similarity
Matches 225; Conserv

100.0%; llarity 100.0%; Conservative 0;

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Score 1238; DB 7; Pred. No. 4.7e-106; ; Mismatches 0;

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RESULT 1
US-11-170-653-24
; Sequence 24, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:

ALIGNMENTS

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APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Alt
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
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APPLICANT: Sibbesen, Ole

APPLICANT: Sorensen, Jens

TITLE OF INVENTION: Xylanse Variants Having Altered Sen

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

CURRENT FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOPTWARE: PatentIn version 3.0
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Matches
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                                                                                                                                                                                                                                                                                                            Altered Sensitivity to
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; LENGTH: 221
; TYPE: PRT
; ORGANISM: C.
; ORGANISM: C.
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APPLICANT: Danisco A/S

APPLICANT: Sibbesen, Ole

APPLICANT: Sorensen, Jens

TITLE OF INVENTION: Xylanse Variants Having

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

CURRENT FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0

; SEQ ID NO 22

LENGTH: 227
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US-11-170-653-22
; Sequence 22, Application US/11170653
; Publication No. US20050271769A1
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                                                                                                                                            ATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPL 115
                                                            IEYYVVENFGTYDPSSQATVKGSVTADGSSYKIAQTQRTNQPSIDGI
 RSSGSVNMKTHFDAWAAKGMKL-GTHNYQIVATEGY
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Pred. No. 1.
                                                                                                                                                                                                                                                                      Score 775.5; DB 7; Pred. No. 7.4e-64;
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APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhil
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.7
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOPTWARE: PatentIn version 3.0
SEQ ID NO 26
LENGTH: 231
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/ Sequence 25, Application US/11170653
/ Publication No. US20050271769A1
/ GENERAL INFORMATION:
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APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Al
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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Matches
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ORGANISM: C.
S-11-170-653-26
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Sequence 26, Application US/11170653
Publication No. US20050271769A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGSAQYTMGEGSRYSVTWRNTGNFVGGKGWNPG-TGRVINYGGAFNPQGNGYLAVYGWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITV 221
                                                                                                                                                                                                                                                                   Altered Sensitivity to
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; LENGTH: 219
; TYPE: PRT
; ORGANISM: C. (
US-11-170-653-29
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; TYPE: PRT
; ORGANISM: C.
; ORGANISM: C.
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US-11-170-653-29
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APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having All
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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Best Local Similarity 57.4
Matches 132; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 29
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Best Local (
                                                                                                                                                                                                                                                                               Matches
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APPLICANT: Sibbesen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSV 171
SGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVA
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                                                        YYIVESFGTYDPSSQASKFGTIQQDGSTYTIAKTTRVNQPSIEGTST
                                                                                YYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQT
                                                                                                                               YQNGAGGSYSVQWQNCGNFVGGKGWNPGA-ARTINFSGTFSPQGNGY
                                                                                                                                                                                                       MVSFKAL---LLGAAGALAFPF-NVTQMNELVARAGTPSGTGTNNGYFYSFWTDGGGTVN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNPLVEYYVIESYGTYNPSSGAQIKGSFQTDGGTYNVAVSTRYNQPSIDGTRTFQQYWSV 179
                                                                                                                                                                 YTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTOKRVGGSVNMONHFNAWSRYGLNL-GOHYYQIVATEGYQSSGSSDIYV 228
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                                                                                                                                                                                                                                                                                                 55.9%; Score 691.5; DB 7; 59.1%; Pred. No. 3.2e-56;
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                                                      FDQFWSVRQNHRS 175
                                                                                         FDOYWSVRODKRT 177
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|AIYGWTQNPLVE 115
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4; Gaps

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RESULT 8
US-11-170-653-27
; Sequence 27, Applicat
; publication No. US200
; GENERAL INFORMATION:
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US-11-170-653-35
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APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Al
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
                                                                            APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Al-
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
                                                                                                                                                                                                                                                                           Sequence 35, Application US/11170653 Publication No. US20050271769A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 126, Conser
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SEQ ID NO 27
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                                              PRIOR APPLICATION NUMBER: GB 0005585.5 PRIOR FILING DATE: 2000-03-08
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TYPE: PRT
               APPLICATION NUMBER: GB 0015751.1 FILING DATE: 2000-06-27
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55.8%; Pred. No. 5.2e-56;
tive 31; Mismatches 62;
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; TYPE: PRT
; ORGANISM: T.
US-11-170-653-31
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FILE OF INVENTION: Xylanse Variants Having All
FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

CURRENT FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08
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SEQ ID NO 35
LENGTH: 241
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Best Local Similarity
Matches 132; Conser
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Best Local :
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APPLICANT: Sibbesen, (
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NUMBER OF SEQ ID NOS: 66
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                                                                                                   TNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVNMAAHFNAWAAAGLQL-GTHDYQIVATEGYYSSGSATVNV
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                                                   YIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTS 178
GTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVA
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                                                                                                                                                                                                                                                               55.3%;
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59.5%; Pred. No. 6.1e-56;
live 31; Mismatches 55
                                                                                                                                                                                                                                               Score 684.5; DB 7;
Pred. No. 1.4e-55;
2; Mismatches 61;
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     222
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|:|||||:||:
|QFWSVRQNKRSGG 178
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                                                                                                                                                                                                                                                                                    223;
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RESULT 12
US-11-170-653-32
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; ORGANISM: T.
US-11-170-653-30
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US-11-170-653-30
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SEQ ID NO 30
LENGTH: 223
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Best Local Similarity 56.2
Matches 126; Conservative
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APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2000-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
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SOFTWARE: PatentIn version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTS 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
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; TYPE: PRT
; ORGANISM: S.
US-11-170-653-23
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ITILE OF INVENTION: Xylanse Variants Having
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
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US-11-170-653-23
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; ORGANISM: T.
US-11-170-653-32
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Best Local Similarity
Matches 128; Conserv
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SOPTWARE: PatentIn ver
SEQ ID NO 32
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Best Local Similarity
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APPLICANT: Sibbesen,
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                                                                                         TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGG)
                                                 RVNAPSIDGTQTFDQYWSVRQDKRT----SGTVQTGCHFDAWARAGLNVNGDHYYQIVA 207
                                                                                                                                                                     TPSSTGTDGGYYYSWWTDGAGDATYONNGGGSYTLTWSGNNGNLVGGKGWNPGAASRSIS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YIVBNFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTS 178
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No. US20050271769A1
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                                                                                                                                                                                                                                                              53.6%; Score 663; DB 7; 61.3%; Pred. No. 1.2e-53;
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                                                                                                                                                                                                                                              26;
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                                                                                                                                                                                                                                              Mismatches
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ivity to Xylanase Inhibitor:

KGWNPGLNARAIH 92

6; Gaps

NLGSEHNYQIVA 184

22

YSYWNDGHGGVTY 59

SWWSDGGAQATY 58

Gaps

22;

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RESULT 15
US-11-170-653-28
; Sequence 28, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
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US-11-170-653-44
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APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Alt
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
APPLICANT: Danisco. A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
ITILE OF INVENTION: Xylanse Variants Having All
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
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ORGANISM: A.
S-11-170-653-44
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Best Local Similarity 56.1%;
Matches 125; Conservative 34
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LENGTH: 221
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APPLICANT: Danisco A/S
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                                                                                                                                                                                                                                                                                                                                                                                                                   TEGYFSSGYARITV
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                                                                                                                                                                     Sensitivity
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 233
; TYPE: PRT
; ORGANISM: M. grisea
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pulp Thermomyces Modified xylanase; Thermomyces WO200192487-A2. 16-MAY-2002 AAE18456; 06-DEC-2001 AAE18456 standard; protein; 194 manufacture; lanuginosus. lanuginosus xylanase, (first poultry; thermostability; alkalophilicity; poultry; swine feed; enzyme; Xyn. entry) \$ χ Έ indu ıstrial process;

The present invention relates to a modified xylanase exhil thermostability and alkalophilicity. Modified xylanase is industrial process such as pulp manufacturing. Modified xy useful for bleaching of pulp, processing of precision devimproving digestibility of poultry and swine feed. Modificing improved performance at conditions of high temperature and exhibits improved thermophilicity and/or alkalophilicity corresponding native xylanase. The present sequence is The lanuginosus xylanase, Xyn

Sequence 194 AA;

WPI;

2002-171435/22.

Sung

31-MAY-2000;

2000US-0213803P.

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31-MAY-2001; 2001WO-CA000769

Modified xylanase exhibiting increased thermostability alkalophilicity useful for industrial processing e.g. 1 manufacturing.

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Disclosure; Page 83-84; 109pp;

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                                                                                                                                              This sequence represents the xylanase from Thermomyces lanuginosus strain DSM 4109. This xylanase, and xylanases derived from Humicola, Thermoascus, Chaetomium, Mucor, Talaromyces, Malbranchea, Myceliophthora, Thielavia, Byssochlamus or Paecilomyces strains can be used in the monocomponent xylanase preparations of the invention. The xylanase preparations and the recombinant Thermomyces xylanase are useful as animal feed additives, which promote in-vivo breakdown of plant cell wall material and thus improve digestibility, growth rate and/or feed
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Byssochlamus; Paecilomyces; animal
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RESULT 3
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PF 11-A
PF 11-A
XX I1-A
XX I1-A
XX II-A
XX I
                                            The sequence represents an endo-1,4-beta-D-xylanase from Thermomyces lanuginosus (Humicola lanuginosa), which may be used as a breadimproving additive. The enzyme may be expressed recombinantly from a plasmid pYES2.0 vector in Saccharomyces cerevisiae DSM 10133 (claimed), and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour, optionally along with other enzymes (amylase, maltogenase, lipase, cellulase, hemicellulase, pentosanase, glucose- oxidase, laccase, protease and/or peroxidase). The enzyme combines particularly well with amylolytic enzymes, and may be used to improve baking properties of flour and/or dough, by increasing volume and improving texture, flavour, crumb softness, freshness and anti-staling properties, while improving dough machinability and stability. (Updated on 16-OCT-2003 to standardise OS field)
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bread improving alpha-amylase, i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermomyces lanuginosus;
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22-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contg. xylanase i volume, improves
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anti-staling properties etc.
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es cerevis
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Query Match Best Local

Similarity

100.0%;

Score Pred.

1088; No. 2

DB 2; .2e-98;

Length

225;

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RESULT 4
ABR63119
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Best Local Similarity 100.0%;
Matches 194; Conservative
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                                                                                                                                              The present sequence is the protein sequence of a thermostable xylanase of Thermomyces lanuginosus. The xylanase has a melting temperature (Tm) of 75.0 degrees C at pH 7.0. It is preferred for use in a claimed composition of the invention, which comprises at least 2 thermostable enzymes selected from an endoglucanase, xylanase, phytase, protease, galactanase, mannanase, dextranase and alpha-galactosidase. The composition is useful for improving the nutritional value of animal feeds, especially those containing soya, wheat, barley, oats and/or rye
                                                                                                                                                                                                                                                                                                                                                                                                                            Composition useful as an animal feed additive comprises at least two thermostable enzymes selected from endoglucanase, xylanase, phytase, protease, galactanase, mannanase, dextranase and alpha-galactosidase
                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
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Score 1088; DB 7;
Pred. No. 2.2e-98;
Mismatches 0;
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QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVG

Query Match Best Local Matches

al Similarity 194; Conser

100.0%; larity 100.0%; Conservative (

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GKGWNPGLNARAI 60

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               enhanced filterability and/or improved extract yield after filtration) which comprises preparing a mash in the presence of enzyme activities (comprising a xylanase of GH family 10 at at least 15% w/w of the total xylanase and endoglucanase enzyme protein) and filtering (A) to obtain a wort. Also described is a composition is useful for reducing the viscosity of an aqueous solution comprising a starch hydrolysate, which is a mash for beer making or a feed composition. The process is useful for the production of an alcoholic beverage, such as beer or whiskey and the composition is useful in the mashing and filtration step in brewing process. The present sequence represents a xylanase used in the mashing process of the invention.
                                                                                                                                                                                                     presence o
Sequence
                                                                                                                                                                                                                 Preparation of a mash (having enhanced filterability and extract yield after filtration) comprises preparing a margresence of enzyme activities comprising xylanase of GH
                                                                                                                                                                                                                                                                                                                                                              17-DEC-2004;
                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2005
                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                          Festersen
                                                                                                                                                                                                                                                                                                                                        19-DEC-2003; 2003DK-00001895
                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              feedstuff; alcohol; fermentation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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                                                                                                                                                                               68pp;
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ash in the
family 10 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ing; filtration.
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                                                                                                                                                                                                                                                                                          ensen LLH;
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RESULT 6
AAB48543
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XX AAB4
XX O5-N
XX Ther
XX Bact
KW Bact
KW Blee
XX Ther
XX Ther
XX Ther
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XX I2-N
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                                                                                                            Query Match
Best Local S
Matches 193
                                                                                                                                                                                             The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp
                                                                                                                                                                                                                                                                                                                                     Non naturally occurring XA protein with enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring Bacillus circulans xylanase is used in an agent for bleaching pulp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial; Bacillus bleaching agent.
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                                                                                                                                                                                                                                                                                                           Disclosure;
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                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                         Bentzien JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermomyces lanuginosus
                                                                                                            / Match 99.5%; So
Local Similarity 100.0%; 1
les 193; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSSGYARITVADVG
                                                     TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH
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                   FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT
                                                                                                                                                                                                                                                                                                           Fig 16L; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lanuginosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     circulans; xylanase; xylanase activity; XA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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                                                                                                           Score 1083; DB 3;
Pred. No. 5.5e-98;
); Mismatches 0;
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                                                                                                                                     Length 194;
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RESULT 7
AAO18649
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XX YJa
KW XYJa
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XX Ther
XX YO2(
XX Ther
XX O9-1
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PF O9-1
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                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a non-naturally occurring xylanase activity (XA) protein comprising an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase, where the protein has been modified to exhibit enhanced thermophilicity, clarations at least 5 amino acid substitutions. A circulans xylanase, and has at least 5 amino acid substitutions. A cleaching agent comprising a modified xylanase is useful for bleaching bleaching juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of the digestibility of feedstuffs and in the washing of super precision devices and semiconductors. The present sequence is a xylanase protein described in the exemplification of the invention
                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xylanase activity; enzyme; thermostable; xylanase; pulp liquid clarification; coffee extraction; plant oil extra starch extraction; food thickener; animal food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel xylanase activity in food and animal feed alkalophilicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermomyces lanuginosus.
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                                                                                                                                                                                                                                                                                                           Sequence 194 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bentzien J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-NOV-2000; 2000US-00710050.
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                                                                                                                                                                                                 193;
                                                                                                                                                                                                                             Similarity
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                                                                                    TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH 61
                            FEGVYOPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 16L;
                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121pp; English.
                                                                                                                                                                                                                           99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein, useful in bleaching process of pulp and industry, has enhanced thermostability and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194
                                                                                                                                                                                                 0;
                                                                                                                                                                                               Score 1083; DB 5;
Pred. No. 5.5e-98;
D; Mismatches O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                     Indels
ECDGSIYRLGKTT
                                                                                                                                                                                                                                                              194;
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RESULT 8
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                                                                                                                                                                                                                                                           The invention relates to a mutant xylanase activity (XA, endo-1,4-beta Xylanase from Bacillus circulans) protein appearing as ADI66730. Also included is a bleaching agent comprising the XA protein. The non-constitutions as compared to Bacillus circulans xylanase ADI66728. The amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64, 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30, 53, or 144. The non-naturally occurring xylanase activity (XA) protein is useful for bleaching pulp in the paper and related industries, but is also useful in the food and animal feed industries. The new protein is crive at higher pH and temperature ranges than naturally occurring xylanases, simplifying incorporation of the xylanase treatment step into pulp processing, especially where the enzyme is added after hot alkali treatment. The present sequence is a xylanase from another species included for comparison.
                                                                                                     Query Match
Best Local S
Matches 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mutant xylanase (XA) substitutions as compared bleaching (paper) pulp, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bentzien J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAY-1999;
07-JUN-1999;
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                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (XENC-) XENCOR
                                                                                                         Local Similarity
168 193, Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp; industry; food; animal feed; thermostability; alkalinophilic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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                                                                                                                                                                                                                     194 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATBGYF
                                 TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEGVYQPNGNSYLAVYGWTRNPLVBYYIVBNFGTYDPSSGATDLGTVECDGSIYRLGKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      c xylanase (XA) protein comprising at least four amino acid lons as compared to Bacillus circulans xylanase, useful for (paper) pulp, and in the food and animal feed industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment.
                                                                                                     99.5%;
llarity 100.0%;
Conservative (
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99US-0138156P.
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                                                                                                     Score 1083; DB 8;
Pred. No. 5.5e-98;
D; Mismatches 0;
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RESULT 9
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                                                                                                                                               Query Match
Best Local S
Matches 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacterial; I
bleaching aq
                                                                                                                                                                                                                         The present sequence is given in a specification relating naturally occurring xylanase activity (XA) proteins. The comprise an amino acid sequence less than 97% identical toccurring Bacillus circulans xylanase. They are modified enhanced thermophilicity, alkalophilicity or thermostabil the naturally occurring B. circulans xylanase. They may k active compound in a bleaching agent which is used for bl
                                                                                                                                                                                                                                                                                                                                                           Non naturally occurring XA protein with enhanced thermopl alkalophilicity or thermostability relative to the natura Bacillus circulans xylanase is used in an agent for blead
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                     Disclosure;
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                                                                                                                                                Local Similarity
les 169; Conserv
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 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGD
                                        TTPNSEGWHDGYYYSWWSDGGGDSTYTNNSGGTYEITWGNGGNLVGGI
                                                                                                                  TTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus circulans; xylanase; xylanase
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                                                                                                                                              88.7%;
llarity 87.6%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                    114pp; English.
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                                                                                                                                              Score 965; DB
Pred. No. 2.2e
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                              ative to the naturally occurr
an agent for bleaching pulp.
                                                                                                                                                            DB 3;
                                                                                                                                                                      Length 194;
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ay be used as the
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e XA proteins
to a naturally
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DHYYQIVATEGYF 181
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ally occurring
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                                                                                              KGWNPGLNARAIH 61
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                                                                                                           Query Match
Best Local :
                                                                                                                                                                     alkalophilicity, or thermostability relative to naturally occurring B. circulans xylanase, and has at least 5 amino acid substitutions. A bleaching agent comprising a modified xylanase is useful for bleaching pulp, in the bioconversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision devices and semiconductors. The present sequence is a xylanase protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                       Novel xylanase activity in food and animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200238746-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching; liquid clarification; coffee extraction; plant oil extraction; starch extraction; food thickener; animal food additive; mutant; m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P variotii xylanase
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                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
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                                                                                              al Similarity
169; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSGYARITVADVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYNAPSIDGTQTFNQYWSVRQDKRSSGTVQTGCHFDAWASAGLNVTGDHYYQIVATEGYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSGYARITVADVG
            FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT
                                               194 AA;
FTGVYQPNGTSYLSVYGWTRNPLVEYYIVENFGSSNPSSGSTDLGTVSCDGSTYTLGQST
                                                                                             88.7%;
llarity 87.6%;
Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                         Fig 16K; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dahiyat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194
                                                                                                                                                                                                                                                                                                                                                                                                             protein, useful in bleaching process of pulp industry, has enhanced thermostability and
                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194
                                                                                              Score 965; DB Pred. No. 2.2e
                                                                                                            DB 5
                                                                                                             -86;
                                                                                                13;
                                                                                                                       Length 194;
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                      xylanase
ss than 97%
                                                                                               0
                                                                                                                                                                                                                                                                                                                          where
                                                                                               Gaps
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121
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정 유

8 8 8

TTPNSEGWHDGYYYSWWSDGGGDSTYTNNSGGTYEITWGNGGNLVGG FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTV

KGWNPGLNARAIH 61
ECDGSIYRLGKTT 121

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AD166750
ID AD16
XX Y1
Expression and AD16
XX AD16
XX AD16
XX AD16
XX AD16
XX Paec
XX AD16
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
               S
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mutant xylanase (XA) protein comprising at least four substitutions as compared to Bacillus circulans xylanase bleaching (paper) pulp, and in the food and animal feed:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADI66750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-118575/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-1999;
07-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6682923-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paecilomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xylanase; xA; EC 3.2.1.8; enzyme; bleaching; bleaching pu
paper industry; food; animal feed; thermostability; alka.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P. variotii xylanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI66750
                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (XENC-) XENCOR.
                                                                                                                                                                                                  included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alkali treatment.
                                                                  169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RYNAPSIDGTQTFNQYWSVRQDKRSSGTVQTGCHFDAWASAGLNVTGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSGYARITVADVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGI
                                                                                                                                                        194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSGYARITVADVG
TTPNSBGWHDGYYYSWWSDGGAQATYTNLBGGTYEISWGDGGNLVGGKGWNPGLNARAIH 61
                                                                                                                                                                                                  for comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
                                                            88.7%; ilarity 87.6%; Conservative 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     variotii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dahiyat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-00570856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0133714P.
99US-0138156P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO 23; 84pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194
                                                              Score 965; DB 8;
Pred. No. 2.2e-86;
l; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                      Length 1
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ulp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r amino acid
, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHYYQIVATEGYF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linophilic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHYYQIVATEGYF 181
                                                                Gaps
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RESULT 12
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AC AAB48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ś
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non naturally occurring XA protein with enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring Bacillus circulans xylanase is used in an agent for bleaching pulp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 221 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200068396-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cochliobolus carbonum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterial, Bacillus bleaching agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cochliobolus carbonum xylanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB48548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (XENC-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-679800/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
                                                                                                                90
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                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XENCOR
                                                                                                                                                              HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
                                                                                                                                                                                                                                                         QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYBISWGDGGNLVGGKGWNPGLNARAI
TRINOPSIDGIRTPQQYWSVRQNKRSSGSVNMKTHFDAWASKGMNL-GQHYYQIVATEGY
                                             TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
                                                                                                                                                                                                                        ONTPNGEGTHNGCFWSWWSDGGARATYTNGAGGSYSVSWGSGGNLVGGKGWNPG-TARTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSGYARITVADVG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSGYARITVADVG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RYNAPSIDGTQTFNQYWSVRQDKRSSGTVQTGCHFDAWASAGLNVTGDHYYQIVATEGYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 16Q;
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000WO-US013172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         circulans; xylanase; xylanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                          68.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114pp; English.
                                                                                                                                                                                                                                                                                                                                22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 AA.
                                                                                                                                                                                                                                                                                                                                                      Score 742; DB 3;
Pred. No. 2.2e-64;
                                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                            SQSQNKGTVTSDGSSYKIAQS
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity;
                                                                                                                                                                                                                                                                                                                              22
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                              120
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                                                                                                            149
                                                                                                                                                                                                                      89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                          60
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8 8 8 8 8

121

TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180

HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVBCDGSIYRLGKT 120

PSSQSQNKGT

TSDGSSYKIAQS 149

TYSGTYNYNGNSYLAVYGWTRNPLVEYYVVENFGTYD

Query Match Best Local S Matches 133

Similarity

68.2%;

Score 742; DB 5; Pred. No. 2.2e-64; 2; Mismatches 33

Length 2:

21;

Conservative

22;

31

QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGG | | | | | | | : | ::|||||||| | | | : | :||| | |||| |||| QNTPNGEGTHNGCFWSWWSDGGARATYTNGAGGSYSVSWGSGGNLVGG

KGWNPG-TARTI

89

KGWNPGLNARAI 60

2;

Gaps

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                       The present invention relates to a non-naturally occurring x activity (XA) protein comprising an amino acid sequence less identical to a naturally occurring Bacillus circulans xylana protein has been modified to exhibit enhanced thermophilicit alkalophilicity, or thermostability relative to naturally occirculans xylanase, and has at least 5 amino acid substituti bleaching agent comprising a modified xylanase is useful for pulp, in the bioconversion of lignocellulosic materials to fice clarifying juice and wine, extracting coffee, plant oils and producing food thickeners, altering texture in bakery product improving the quality of dough, helping bread to rise and production the digestibility of feedstuffs and in the washing of sup devices and semiconductors. The present sequence is a xylana classification of the invention
                                                                                                                                                                                                                                                                                           Novel xy in food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xylanase activity; enzyme; thermostable; xylanase; pulp liquid clarification; coffee extraction; plant oil extra starch extraction; food thickener; animal food additive;
   Sequence 221
                                                                                                                                                                                                                                                                           in food and animal alkalophilicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cochliobolus carbonum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C carbonum xylanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAO18654 standard; protein; 221
                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                            Bentzien J,
                                                                                                                                                                                                                                                                                                                                                                                                                                           09-NOV-2001; 2001WO-US048018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAO18654;
                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-2000; 2000US-00710050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200238746-A2
                                                                                                                                                                                                                                                                                                                                                                                        (XENC-) XENCOR INC
                                                                                                                                                                                                                                                                                                                                   2002-608200/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                           xylanase activity od and animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSTGNAQITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSSGYARITV
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   A
A
                                                                                                                                                                                                                                                                                                                                                              Dahiyat
                                                                                                                                                                                                                                                  160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
                                                                                                                                                                                                                                                  121pp;
                                                                                                                                                                                                                                                                                       protein, useful in bleaching process of pulp and industry, has enhanced thermostability and
                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pulp |
extra
                                       roducts, e.g.
nd processing of
d additives to aid
f super precision
ylanase protein
                                                                                                                                                                                           lanase, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bleaching;
                                                                                                                                                    tutions. A
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                                                                                                                                                                                                          ng xylanase
less than 97%
                                                                                                         and starch,
                                                                                                                         for bleaching o fuels, for
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                                                                                                                                                                occurring B.
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RESULT 14
AD166756
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                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 133; Conser
                                                                                                                                                                                                                                                                                                                                                       xylanase from Bacillus circulans) protein appearing as mincluded is a bleaching agent comprising the XA protein. The non-
naturally occurring XA protein comprises at least four amino acid
substitutions as compared to Bacillus circulans xylanase ADI66728. The
amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,
79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,
58, or 144. The non-naturally occurring xylanase activity (XA) protein is
useful for bleaching pulp in the paper and related industries, but is
also useful in the food and animal feed industries. The new protein is
active at higher pH and temperature ranges than naturally occurring
xylanases, simplifying incorporation of the xylanase treatment step into
pulp processing, especially where the enzyme is added after hot alkali
treatment. The present sequence is a xylanase from another species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New mutant xylanase (XA) protein comprising at least four amino acid substitutions as compared to Bacillus circulans xylanase, useful for bleaching (paper) pulp, and in the food and animal feed industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. carbonum xylanase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-118575/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAY-1999;
07-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6682923-B1.
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                                                                                                                                                                                                                                                                                                               Sequence
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TRTNQPSIDGTRTFQQYWSVRQNKRSSGSVNMKTHFDAWASKGMNL-GQHYYQIVATEGY
                                                                                                                                  221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSSGYARITY 190
                                                                                                         QNTPNGEGTHNGCFWSWWSDGGARATYTNGAGGSYSVSWGSGGNLVGGKGWNPG-TARTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relates to a mutant xylanase activity Bacillus circulans) protein appearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates to
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99US-0138156P.
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                                                                                                                                                                                                                                  68.2%;
70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme; bleaching; bleaching pulp;
wal feed; thermostability; alkalinophilic;
                                                                                                                                                                                                            22;
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                                                                                                                                                                                                          Score 742; DB Pred. No. 2.2e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  xylanase activity (XA, endo-1,4-beta protein appearing as ADI66730. Also prising the XA protein. The non-
                                                                                                                                                                                                                                  DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             animal feed industries.
                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                          Length
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YSGTYOPNGNSYLSVYGWTRSSLIEYYIVESYGSYDPSSAASHKGSY

TCNGATYDILSTW 122

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RESULT 15
AAW60736
XX AAW60
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XX Famil
KW Famil
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                                                                                                                                                                 Query Match
Best Local Similarity
Matches 119; Conseru
                                                                                                                                                                                                                                                                                                                         AAW60728-44 represent family 11 xylanases. The specication describes a method for modifying a Family 11 xylanase to improve its thermophilicity, alkalophilicity and or thermotolerance. This method comprises modification of amino acids 10, 27 or 29 of Trichoderma reesei xylanase II or corresponding aligned amino acids of another Family 11 xylanase, replacement of one or more amino acids sequences in the N-terminal region with corresponding aligned sequences from another Family 11 xylanase to form a chimeric xylanase and/or upstream extension of the N terminus by addition of upto 10 amino acids. The modified xylanses are useful for improving the bleachability of wood pulp by treatment at 55-75 degrees celsius and pH 7.5-9.0 for 5-180 minutes. They might also be useful as digestibility-improving animal feed additives. They might also be useful in the processing of wheat or maize for starch production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Family 11 xylanase; improve; thermophilicity; alkalopl thermotolerance; bleach; wood pulp; processing; wheat digestibilitiy-improving animal feed additive; starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gung
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                                                                                                                                                                                                                                                                           Sequence
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                                                                                       TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGWNPGLNARAIH 61
      FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTV
                                                            TPSSTGTDGGYYYSWWTDGAGDATYQNNGGGSYTLTWSGNNGNLVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yaguchi M,
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 40;
                                                                                                                                                                                                                                                                             AA,
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                                                                                                                                                                     Score 663; DB 2;
Pred. No. 1.1e-56;
5; Mismatches 43
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                                                                                                                                                                                                                     Length
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|KGWNPGAASRSIS 62
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            ECDGSIYRLGKTT 121
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| Search co Job time | DЬ | ş | Вb | 8 |
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| Search completed: February 10, 2006, 14:54:12 Job time : 130.568 secs | 183 TEGYQSSGTATITV 196 | 177 TEGYPSSGYARITV 190 | 123 RYNAPSIDGTQTFEQFWSVRNPKKAPGGSISGTVDVQCHFDAWKGLGMNLGSEHNYQIVA 182 | 122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVA 176 |

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Regult
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution.
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2: pir2:*
3: pir3:*
4: pir4:*
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1088
1 QTTPNSEGWHDGYYYSWWSN
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endo-1,4-beta-xylanase (EC 3.2.1.8) A - bracket fungus (Schizophy N;Alternate names: xylanase A C;Species: Schizophyllum commune C;Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change C;Accession: A44597; S41411; A05147; S38973
R;Yaguchi, M.
submitted to the Protein Sequence Database, March 1994
A;Reference number: A44593
A;Accession: A44597
A;Molecule type: protein A;Residues: 1-197
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ALIGNMENTS

(Schizophyllum commune)

ge 09-Jul-2004

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A; Molecule type: protein
A; Residues: 1-27 < PAI>
A; Cross-references: UNIPARC:UPI0000172967
A; Cross-references: UNIPARC:UPI0000172967
R; Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Campbell, R.; Ya FEBS Lett. 334, 296-300, 1993
A; Title: Amino acid sequence and thermostability of xylanase A fr A; Reference number: S38973; MUID:94063044; PMID:8243636
A; Accession: S38973
A; Molecule type: protein
A; Residues: 1-197 < OKU>
A; Cross-references: UNIPARC:UPI000034D33
A; Experimental source: ATCC 38548
C; Function:
A; Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bon A; Pathway: xylan degradation
C; Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase hom C; Keywords: extracellular protein; glycosidase; hydrolase; polysa F; 12-197/Domain: endo-1,4-beta-xylanase homology < XYL>
F; 87,184/Active site: Glu #status predicted
F; 111-160/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT: p35809; UNIPARC: UPI0000034D33
A;Experimental source: strain Delmar ATCC 38548
R;Bray, M.R.; Clarke, A.J.
Bur. J. Biochem. 219, 821-827, 1994
A;Title: Identification of a glutamate residue at the active A;Reference number: S41411; MUID: 94155888; PMID: 7906649
A;Accession: S41411
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 83-123 < BRA>
A; Cross-references: UNIPARC: UPI0000172966
R; Paice, M.G.; Jurasek, L.; Carpenter, M.R.;
Appl. Environ. Microbiol. 36, 802-808, 1978
A; Reference number: A05147; MUID: 79102289; PN
A; Accession: A05147
    Query Match
Best Local Similarity
Matches 119; Conserv
                                 60.9%;
Score 663; DB
Pred. No. 5e-4
26; Mismatches
                                 663; DB 1
No. 5e-47;
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lysaccharide degradation
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Conservative

3

Indels

6

Gaps

2;

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endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile (;Species: Chaetomium gracile C;Date: 09-Dec-1997 #sequence revision 09-Dec-1997 #text_change 05 C;Accession: $71472; $78206 R;Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N. Curr. Genet. 29, 73-80, 1995 A;Title: Two family G xylanase genes from Chaetomium gracile and t A;Reference number: $71472 A;Accession: $71472 A;Accession: $71472 A;Accession: $71472 A;Accession: $71472 A;Accession: $71472 A;Accession: $78206 A;Ac
RESULT 3
S57477
endo-1,4-beta-xylanase (EC :
N;Alternate names: xylanase
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Pred. No. 2.
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                           precursor
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crospecies: Humicola insolens
C;Species: Humicola insolens
C;Species: Humicola insolens
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 0
C;Accession: S43919
R;Dalboge, H.; Heldt-Hansen, H.P.
Mol. Gen. Genet: 243, 253-260, 1994
A;Title: A novel method for efficient expression cloning of funga
A;Reference number: S43919
A;Molecule type: mRNA
A;Residues: 1-227 <DAL>
A;Cross-references: UNIPROT: P55334; UNIPARC: UPI0000421A4; EMBL:X
C;Genetics:
A;Gene: XYL1
C;Function:
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase hom
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-19/Domain: signal sequence #status predicted <SIG-F;20-227/Product: endo-1,4-beta-xylanase #status predicted <MAT>
F;48-225/Domain: endo-1,4-beta-xylanase homology <XYL>
F;112,123,157/Binding site: substrate (Tyr, Tyr, Arg) #status predicted
F;121,212/Active site: Glu #status predicted
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C;Function:
A;Description: catalyzes the hydrolysis of 1,4-beta.
A;Description: catalyzes the hydrolysis of 1,4-beta.
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-C;Keywords: glycosidase; hydrolase; polysaccharide of C;Keywords: signal sequence #status predicted of C;1-19/Domain: signal sequence #status predicted of C;20-225/Product: endo-1,4-beta-xylanase 1 #status predicted of C;48-225/Domain: endo-1,4-beta-xylanase homology of C;121,212/Active site: Glu #status predicted
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A;Description: Expres
A;Reference number: S
A;Accession: S57477
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C;Date: 10-Oct-1999
C;Accession: S5747
R;Perez-Gonzalez,
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A; Residues: 1-225 < PER>
A; Cross-references: UNII
C; Genetics:
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 Local Similarity
nes 113; Conser
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Expression in Saccharomyces ce
mber: S57469
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                  59.4%;
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Pred. No. 9.6e
27; Mismatches
 Score 646; DB Pred. No. 1.4e 7; Mismatches
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                                                                                               predicted
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   Gaps
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Conservative

1

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RESULT 5
$71473
endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Chaetomium gracile
C;Species: Chaetomium gracile
C;Date: O9-Dec-1997 #sequence revision O9-Dec-1997 #text_change O9-Jul-2004
C;Accession: $71473; $78207
R;YOSHin, S:, VAIA73; $78207
R;YOSHin, S:, YAIA73; $78207
R;YOSHin, S:, YAIA73; $78207
R;YOSHin, S:, VAIA73; $78207
R;YOSHine, S:, VAIA73; $78207
R;Title: Two family G xylanase genes from Chaetomium gracile and their expla; Reference number: $71472; MUID:96118924; PMID:8595661
A;Accession: $71473
A;Accession: $71472; MUID:96118924; PMID:8595661
A;Accession: $71473
A;Molecule type: DNA
A;Residues: 1-241 <YOS>
A;Cross-references: UNIPARC:UPIO000421AB; EMBL:D49851; NII
A;Accession: $78207
A;Molecule type: protein
A;Residues: 38-44;89-91;153-161 <YOH>
A;Cross-references: UNIPARC:UPIO000175A77; UNIPARC:UPIO000175A78; UNIPARC:C;Genetics:
A;Introns: 88/2
C;Genetics:
A;Introns: 88/2
C;Genetics:
A;Jathaway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Superfamily: endo-1,4-beta-xylanase B #status predicted <MAT>
F;31-241/Product: endo-1,4-beta-xylanase B #status predicted <MAT>
F;116,207/Active site: Glu #status predicted
Fills,207/Active site: Glu #status predicted
RESULT 6
A44593
endo-1,4-beta-xylanase (
N;Alternate names: xylan
C;Species: Trichoderma h
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                                                                                                                                                                                                                                                                                                        IHFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI
                                                                                                                                                                                                                                                                                                                                                                QTLTSSQTGTNNGYYYSFWTDGQGNVQYTNEAGGQYSVTWSGNGNWVGGKGWNPG-SART
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No. 2.9e-45;
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                                         (Trichoderma
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A;Residues: 1-190 <YAG>
A;Cross-references: UNIPARC:UPI0000493CB
A;Cross-references: UNIPARC:UPI0000493CB
A;Experimental source: strain E58
R;Campbell, R.L.; Rose, D.R.
submitted to the Brookhaven Protein Data Bank, June 19
A;Reference number: A52868; PDB:1XND
A;Contents: annotation; X-ray crystallography, 1.8 ang
C;Function:
A;Description: catalyzes the hydrolysis of 1,4-beta-xy
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-x
C;Keywords: glycosidase; hydrolase; polysaccharide deg
F;12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
F;86,177/Active site: Glu #status experimental
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A;Reference number: 1
A;Accession: A44593
A;Molecule type: prot
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C;Accession:
R;Yaguchi, M.
                                                                                                          A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic A;Pathway: xylan degradation C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;12-190/Domain: endo-1,4-beta-xylanase homology <XYL> F;86,177/Active site: Glu #status predicted F;126-127/Cleavage site: Pro-Ser (unidentified proteinase) #st F;129-130/Cleavage site: Glu-Gly (unidentified proteinase) #st
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                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-190 <YAG>
A;Cross-references: UNIPROT:Q7M520;
C;Function:
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A44595
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QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 60
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                                       27;
                                Score 636.5; I
Pred. No. 6.9e
27; Mismatches
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Pred. No. 6.9e-45;
7; Mismatches 47
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lysaccharide degradation
                                     3636.5; DB 1;
. No. 6.9e-45;
ismatches 48;
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                                      1; Gaps
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xylanase 1 - fungus (Trichoderma reesei)
C; Species: Trichoderma reesei
C; Date: 19-Mar-1997 #sequence_revision 09-May-1997 #te
C; Accession: S39154
R; Toerroenen, A.; Mach, R.L.; Messner, R.; Gonzalez, R
Biotechnology 10, 1461-1465, 1992
A; Title: The two major xylanases from trichoderma rees
A; Reference number: S39154
A; Accession: S39154
A; Accession: S39154
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-222 < TOE>
A; Cross-references: UNIPROT: p36217; UNIPARC: UPI000042
C; Genetics:
A; Gene: xyn1
A; Introns: 90/2
C; Superfamily: endo-1, 4-beta-xylanase; endo-1, 4-beta-x
F; 44-222/Domain: endo-1, 4-beta-xylanase homology < XYL>
A; Molecule type: DNA
A; Residues: 1-223 < SAA>
A; Cross-references: UNI
                                            R;Saarelainen, R.; Paloheimo, M.; Fagerstromol. Gen. Genet. 241, 497-503, 1993
A;Title: Cloning, sequencing and enhanced enhances. S39883; MUID:94088442; A;Accession: S39883
                                                                                                                   endo-1,4-beta-xylanase (EC 3.2.1.8) II precursor - N;Alternate names: endoxylanase II C;Species: Trichoderma reesei C;Date: 19-Mar-1997 #sequence revision 19-Mar-1997 C;Accession: S39883; S39884
                                                                                                                                                                                               RESULT
S39883
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S39154
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                                                                                                                                                                                                                                                            PSSGSASITVS
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1: endo-1,4-beta-xylanase homology <XYL>
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   UNIPROT: Q02244;
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Pred. No. 9.9e-45;
8: Mismatches 47;
                                                                                                         Fagerstroem,
    UNIPARC: UPI00000421A8;
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                                                             expression of 
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    EMBL:S67387;
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                                                                              Trichoderma
                                                                                                        P.L.;
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   NID: g455906;
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submitted to the Prot
A;Reference number: J
A;Accession: A44594
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A;Gene: xin2
A;Introns: 91/2
C;Function:
A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylosescription: catalyzes the hydrolase; polysaccharide degradation cyclosescription: glycoprotein; glycosidase; hydrolase; polysaccharide degradation figure is signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-33/Domain: propeptide #status predicted <PRO>
F;34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>
F;45-223/Domain: endo-1,4-beta-xylanase homology <XYL>
F;71,94/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;110,121/Binding site: substrate (Tyr) #status predicted
F;110,210/Active site: Glu #status predicted
                                                                                                                                                                                                       A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic A;Pathway: xylan degradation C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;12-190/Domain: endo-1,4-beta-xylanase homology <XYL>F;77,88/Binding site: substrate (Tyr) #status predicted F;86,177/Active site: Glu #status predicted
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A;Accession: S39884
A;Molecule type: protein
A;Residues: 34-43;49-57;121-151;178-191 <SAF>
A;Cross-references: UNIPARC:UPI0000175A7C; UNIC;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-190 <YAG>
A;Residues: 1-190 <YAG>
A;Cross-references: UNIPROT:Q7M519; UNIPARC:UPI0000034D34
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-190 < YAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: xylanase IIA
C;Species: Trichoderma viride
C;Date: 27-Jun-1994 #sequence_revi
C;Accession: A44594
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QTIGPGTGFNNGYFYSYMNDGHGGVTYTNGPGGQFSVNWSNSGNFVGGKGWQPGTKNKVI 60
                                                    QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 60
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er: A44593
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                                                                                                                         58.3%;
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                                                                                                Score 634.5;
Pred. No. 1e-4
27; Mismatches
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Pred. No. 1e-4
8; Mismatches
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endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae
N;Alternate names: endo-1,3-beta-xylanase G2; xylanase G2
C;Species: Aspergillus oryzae
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Ju:
C;Accession: JC7577; PC7120
R;Kimura, T.; Suzuki, H.; Furuhashi, H.; Aburatani, T.; Morimoto, K.;
Biosci. Biotechnol. Blochem. 64, 2734-2738, 2000
A;Title: Molecular cloning, overexpression, and purification of a majonal partition of a majonal partitle in the complexity of the c
                                                                                                                                                                                                                                                                                                   RESULT 12
S57469
endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - Emerice N;Alternate names: xylanase 2 C;Species: Emericella nidulans, Aspergillus nidulans C;Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_C;Accession: S57469
R;Perez-Gonzalez, J.A.
submitted to the EMBL Data Library, June 1995 A;Description: Expression in Saccharomyces cerevisiae of A;Reference number: S57469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: xynG2
A;Introne: 100/2
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase
C;Keywords: glycosidase; hydrolase
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYSGSFNPSGNGYLAVYGWTTDPLIEYYIVESYGTYNPGSGGTYKGQVTSDGGTYNIYTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
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59.58;
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Pred. No. 7.5e-44;
3; Mismatches 47
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A;Molecule type: DNA
A;Residues: 1-221 <PER>
A;Cross-references: UNIPROT:P55333; UNIPARC:UPI0000139075; EMBL:Z
C;Genetics:
A;Introns: 89/3
C;Function:
A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bon
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase hom
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-19/Domain: signal sequence #status predicted <SIG>
F;19-221/Product: endo-1,4-beta-xylanase 1 #status predicted
F;44-221/Domain: endo-1,4-beta-xylanase homology <XYL>
F;117,208/Active site: Glu #status predicted
                                                                                                                                             A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic A;Pathway: xylan degradation C;Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-C;Keywords: extracellular protein; glycosidase; hydrolase; pol F;1-40/Domain: signal sequence #status predicted <SIG>F;41-333/Product: endo-1,4-beta-xylanase B #status experimenta F;54-230/Domain: endo-1,4-beta-xylanase homology <XYL>F;127,217/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endo-1,4-beta-xylanase (EC 3.2.1.8) B p N;Alternate names: xylanase B C;Species: Streptomyces lividans C;Date: 10-Mar-1994 #sequence_revision C;Accession: JS0590; PS0239 R;Shareck, F.; Roy, C.; Yaguchi, M.; Mo Gene 107, 75-82, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Sequences of three A;Reference number: JS0589; A;Accession: JS0590
                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 41-71 <SH2>
A;Cross-references: UNIPARC:UPI000017296B
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A;Accession: PS0239
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C;Function:
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A; Residues: 1-333 <SHA>
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Gene 107, 75-82,
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les 106; Conser
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TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKG
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                                                            52.5%; !
nilarity 55.2%; !
Conservative 24;
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                                                                   24;
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Pred. No. 4.6e-43;
1; Mismatches 47
                                                                Score 571.5; DB 1;
Pred. No. 2.6e-39;
1; Mismatches 59;
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lysaccharide degradation
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                                                                   3; Gaps
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endo-1,4-beta-xylanase (EC 3.2.1.8) - Penicillium sp.
N;Alternate names: endo-1,3-beta-xylanase; xylanase
C;Species: Penicillium sp.
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: JC7307; PC7086
R;Kimura, T.; Ito, J.; Kawano, A.; Makino, T.; Kondo, H.; Karita, S.; Sakka, Biosci. Biotechnol. Biochem. 64, 1230-1237, 2000
A;Title: Purification, characterization, and molecular cloning of acidophili A;Reference number: JC7307
A;Accession: JC7307
A;Accession: JC7307
A;Residues: 1-221 <KIM>
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R;Redenbach, M.; Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kinashi, Mol. Microbiol. 21, 77-96, 1996

A;Title: A set of ordered cosmids and a detailed genetic and physical map for th A;Reference number: Z20556; MUID:97000351; PMID:8843436

A;Recession: T50601

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-335 < RED>
A;Cross-references: UNIPROT:Q9RKN6; UNIPARC:UPI0000DC56E; EMBL:AL133220; PIDN:CA;Experimental source: strain A3(2)

C;Genetics:
A;Gene: xlnB

C;Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homo
C;Keywords: glycosidase; hydrolase
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T50601
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JC7307
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A;Residues: 32-51 <KI2>
A;Cross-references: UNIPARC:UPI0000175A85
C;Genetics:
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XYN1_COCCA
Q9C263_9PEZI
Q51SA1_MAGGR
Q51SA1_MAGGR
Q766V1_9ASCO
XYNA_SCHCO
Q12579_9PEZI
Q13447_COCSA
Q70T28_9PLEO
Q7SDQ1_NEUCR
Q4WG11_ASPFU
Q871E8_NEUCR
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| EMBL; U35436; AAB94633.1; -; Genomic_DNA PDB; 1YNA; X-ray; @=32-225. InterPro; IPR001137; Glyco_hydro_11. Pfam; PF00457; Glyco_hydro_11; 1. PRINTS; PR00911; GLHYDRLASE11. PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 3D-structure; Glycosidase; Hydrolase; Pysignal; Xylan degradation. | s-Prot entry is copyright. It the Swiss Institute of Bioinf ean Bioinformatics Institute. Institute. | EDLINE=98426042; PubMed=9753433; DOI=10 ruber K., Klintschar G., Hayn M., Schla ratky C.; Thermophilic xylanase from Thermomyces ray structure and modeling studies."; chochemistry 37:13475-13485(1998). - CATALYTIC ACTIVITY: Endohydrolysis clinkages in xylans. - BIOPHYSICOCHEMICAL PROPERTIES: Thermostable; Thermostable; PATHWAY: Xylan degradation. - SIMILARITY: Belongs to the glycosylfamily. | SEQUENCE. 5826 / Tsiklinsky; 5826 / Tsiklinsky; 033440; PubMed=8879171; DOI=1 A., Holzmann K., Hayn M., Ste nd characterization of the ge ynA from Thermomyces lanuging nol. 49:211-218(1996). TALLOGRAPHY (1.55 ANGSTROMS). | 7NA_THELA 3097; 30 | ALIGNMEN 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 32 629.5 57.9 220 2 QBJOT4_9HYPO 33 627.5 57.7 223 2 Q7ZBQ3_TRIVI 34 625 57.4 232 2 Q9HFA4_ASPOR 35 623.5 57.3 223 2 Q9HFA4_ASPOR 36 621 57.1 225 1 XYNB_ASPKA 37 620 57.0 221 2 Q5AQR5_EMENI 38 619 56.9 231 2 Q4HVK9_GIBZE 39 619 56.9 231 2 Q4HVK9_GIBZE 40 617 56.7 225 2 QFZA57_GIBZE 41 617 56.7 225 2 QFZA57_GIBZE 41 617 56.7 225 2 QFZA57_GIBZE 42 617 56.7 225 2 QFZA57_GIBZE 43 616 56.6 225 1 XYNZ_ASPNG 44 615 56.5 221 1 XYNZ_MAGGR |
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Kumar P.R., Eswaramoorthy S., Vithayathil P.J., Viswamitra M.A.;
"The tertiary structure at 1.59 A resolution and the proposed amino acid sequence of a family-11 xylanase from the thermophilic fungus
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InterPro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PRINTS; PR00911; GLHYDRLASE11.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.

3D-structure; Acetylation; Direct_protein se Hydrolase; Xylan degradation.

ACT_SITE 86 86 Nucleophile (By ACT_SITE 178 178 Proton donor (B MOD_RES 1 1 1 1 N-acetylglycine DISULFID 110 154

SEQUENCE 194 AA; 20947 MW; 1D5C50AA4F6ED
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OPLEO
PRELIMINARY;

OPUVZ3

OPUVZ3;

O1-MAY-2000 (TrEMBLrel. 13, Cre
O1-MAY-2000 (TrEMBLrel. 13, Las
O1-OCT-2003 (TrEMBLrel. 25, Las
Xylanase precursor.

Name=xyl1;
Setosphaeria turcica.
Eukaryota; Fungi; Ascomycota; P
Pleosporales; Pleosporaceae; Se
NCBI_TaxID=93612;
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J. Mol. Biol. 295:581-593(2000).
-!- CATALYTIC ACTIVITY: Endohydrolysis
linkages in xylans.
-!- BIOPHYSICOCHEMICAL PROPERTIES:
STRAIN=H2;
Degefu Y., Paulin L., Lubeck P.S.;
Pegefu Y., Paulin L., Lubeck P.S.;
Cloning, sequencing and expression of a xy
pathogen Helminthosporium turcicum Pass.";
pathogen Helminthosporium turcicum Pass.";
Eur. J. Plant Pathol. 107:457-465(2001).
EMBL; AJ238895; CAB52417.1; -; Genomic_DNA.
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                                                                                                                                                 NUCLEOTIDE
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- SIMILARITY: Beldiamily.
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Proton donor (By
N-acetylglycine.
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Setosphaeria.
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                                                                                                                           NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

MEDLINE=21654148; PubMed=11795847; DOI=10.1007/s00294-001-0260-0;

A Gomez-Gomez E., Roncero M.I.G., Di Pietro A., Hera C.;

T "Molecular characterization of a novel endo-beta-1,4-xylanase gene
T from the vascular wilt fungus Fusarium oxysporum.";

L Curr. Genet. 40:268-275(2001).

R MBL; AF246830; AAK27974.1; -; Genomic_DNA.

R HSSP; O43097; 1YNA.

R GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; I

R GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; I

R GO; GO:0045493; P:cylan catabolism; IEA.

R InterPro; IPR001137; Glyco_hydro_11.

R Pfam; PF00457; Glyco_hydro_11; 1.

R PRINTS; PR00911; GLHYDRLASE11.

R PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

R PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.

W Xylan degradation.

SEQUENCE 295 AA; 30858 MW; CA441056DCD3C104 CRC64;
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GO; GO:0004553; F:hydrolase activity, hydrolyzing O-QGO; GO:0005975; P:carbohydrate metabolism; IEA.

GO; GO:0045493; P:xylan catabolism; IEA.

InterPro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PRINTS; PR00911; GLHYDRLASE11.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

Signal; Xylan degradation.

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QGC1R2;
Q9C1R2;
Q9C1R2;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update O1-OCT-2003 (TrEMBLrel. 25, Last annotation update O1-OCT-20
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Pred. No. 4.7e-58;
  ore 750; DB 2;
ed. No. 3.2e-57;
Mismatches 29;
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Hypocreales; Fusarium;
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EMBL; L13596; AAA33024.1; -; Genomic_DNA.
HSSP; Q43097; 1YNA.

SMR; Q06562; 31-218.

InterPro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PFANNTS; PR00911; GLHYDRLASE11.

R PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

R PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
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01-FEB-1995 (Rel. 31, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Endo-1,4-beta-xylanase I precursor (EC 3.2.1.
beta-D-xylan xylanohydrolase 1).
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Direct protein sequencing;

Xylan degradation.

SIGNAL 1 30
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Holden F.R., Walton J.D.;
"Xylanases from the fungal maize pathogen entry of the fungal maize pathogen entry of the function. Major xylan-degrading enzyme hydrolysis of arabinoxylan, the major entry of the function."
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STRAIN=Race 1 / Isolate SB111;
STRAIN=94003417; PubMed=8400376;
MEDLINE=94003417; PubMed=8400376;
Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;
"Cloning and targeted gene disruption of XYL1, a beta gene from the maize pathogen Cochliobolus carbonum.";
Mol. Plant Microbe Interact. 6:467-473(1993).
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Pleosporales; Pleosporaceae; Cochliobolus.
NCBI_TaxID=5017;
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                                                                                                                                              Lubeck P.S., Paulin L., Degefu Y., Lubeck M., Collinge "Molecular cloning and DNA sequencing of a xylanase gen phytopathogenic fungus Ascochyta pisi Lib.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases EMBL; Z68891; CAA93120.1; -; Genomic_DNA.
RSP; O43097; 1YNA.
RMR; Q00263; 39-224.
GO; GO:0004553; F:hydrolase activity, hydrolyzing O-gly GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0045493; P:xylan catabolism; IEA.
InterPro; IPR001137; Glyco_hydro_11.
Pfam; PF00457; Glyco_hydro_11.
PROSITE; PR00911; GLHYDRLASE11.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
Signal; Xylan degradation.
Potential.
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263_9PEZI
260_9PEZI PRELIMINARY;
Q00263;
Q00263;
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01-NOV-1996 (TrEMBLrel. 01, L
01-OCT-2003 (TrEMBLrel. 25, L
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Nucleophile (By similarity)
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G -> A (in Ref. 2).
S -> W (in Ref. 2).
S -> W (in Ref. 2).
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13-SEP-2005 (TremBLrel
13-SEP-2005 (TremBLrel
Hypothetical protein.
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Submitted (Oc. [2]
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[3]
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Q51SA1
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Magnaporthe grisea 70-15.
Magnaporthe grisea 70-15.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                 NUCLEOTIDE SEQUENCE.
STRAIN=70-15;
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                     , Brown
                                                                                                          Magnaporthe grisea."; the EMBL/GenBank/DDBJ
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Last annotation updat
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E., Iliev I.,
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K., Hafez N.,
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Best Local S
Matches 125
Query Match 64.8%;
Best Local Similarity 66.5%;
Matches 125; Conservative 7
                                                                           NUCLEOTIDE SEQUENCE.

TISSUE=Mycelium;

Wu S.-C., Darvill A.G., Albersheim P.;

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ database

EMBL; AY144349; AAB06573.2; -; Genomic_DNA.

HSSP; O43097; IYNA.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-;

GO; GO:0005975; P:carbohydrate metabolism; IEA.

GO; GO:0045493; P:xylan catabolism; IEA.

GO; GO:0045493; P:xylan catabolism; IEA.

InterPro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PFAM; PF00457; Glyco_hydro_11; 1.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

Xylan degradation.

SEQUENCE 231 AA; 25305 MW; CECF024A9D5A795B CRC6.
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Q92245;
Q92245;
01-FEB-1997 (TrEMBLrel. 02
01-FEB-1997 (TrEMBLrel. 02
01-OCT-2003 (TrEMBLrel. 25
Endo-beta-1,4-D-xylanase.
Name=XYL4;
                                                                                                                                                                                                                                                                                                                                                                                                                              Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
NCBI_TaxID=148305;
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Submitted (OCT-2003) to
-i- CAUTION: The
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Pred. No. 1.7e
25; Mismatches
                    Score 705;
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Matches 120
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ database EMBL; ABB11442; BAD07040.1; -; Genomic_DNA.

HSSP; P09850; 1BCX.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-996; GO:0005975; P:carbohydrate metabolism; IEA.

GO; GO:0045493; P:xylan catabolism; IEA.

GO; GO:0045493; P:xylan catabolism; IEA.

InterPro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PRINTS; PR00911; GLHYDRLASE11.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

Xylan degradation.

SEQUENCE 235 AA; 25526 MW; C929BE7FD73682CA CRC6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q766V1;
05-JUL-2004
05-JUL-2004
05-JUL-2004
G/11 family ;
Name=sxyl1;
Scytalidium t
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Morinaga T., B
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NCBI_TaxID=85995;
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Pred. No. 6.4e
24; Mismatches
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|WDGATYQVAQSTR 162
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XYNA_SCHCO

STANDARD;

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01-JUN-1994 (Rel. 29, La
01-FEB-2005 (Rel. 46, La
Endo-1,4-beta-xylanase r
xylanohydrolase A).
Name=XXNA;
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Agaricales; Schizophyllaceae; Schizophyllum.
NCBI_TaxID=5334;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL PROTEIN SEQUENCE, AND ACTIVE SITE GLU-87.

STRAIN=ATCC 38548 / Delmar;

STRAIN=ATCC 38548 / Delmar;

MEDLINE=94155888; PubMed=7906649;

Bray M.R., Clarke A.J.;

Bray M.R., Clarke A.J.;

"Identification of a glutamate residue at the active site of xy

A from Schizophyllum commune.";

Eur. J. Biochem. 219:821-827(1994).

-i- FUNCTION: Hydrolyzes xylans into xylobiose and xylose.

-i- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jurasek L., Paice M.G.;
"Amino acid sequence and thermostability
Schizophyllum commune.";
FEBS Lett. 334:296-300(1993).
[3]
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STRAIN=ATCC 38548 / Delmar;
Yaguchi M., Roy C., Ujiie M., Watson D.(
(In) Visser J., Beldman G., Kusters-van
                                                                                                                                   InterPro; IPRO01137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PF1NTS; PR00911; GLHYDRLASE11.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

Direct protein sequencing; Glycosidase; Hydrolase; Xylan ACT_SITE 87 87 Nucleophile (Probable).

ACT_SITE 184 184 Proton donor (By similarity)

DISULFID 111 160

SEQUENCE 197 AA; 20979 MW; 42C8074E67C1FBE9 CRC64;
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STRAIN-ATCC 38548 / Delmar;

MEDLINE-94063044; PubMed-8243636; DOI=10.1016/0014-5793(93)80698-T;

OKU T., Roy C., Watson D.C., Wakarchuk W., Campbell R., Yaguchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xylans and xylanases,
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                Active over a very broad pH range; PATHWAY: Xylan degradation. SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the glycosyl family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pH dependence:
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BIOPHYSICOCHEMICAL PROPERTIES
                                                                                                                                                                                                                                                                        A44597; A44597.
; P81536; 1PVX.
                                                                                                                                                                                                                                                                                                                             Swiss-Prot entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL Buropean Bioinformatics Institute. There are no restrict as long as its content is in no way modified and this states.
  62
                                                                                            Similarity
                         FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT
                                                                                Conservative
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st annotation update)
(EC 3.2.1.8) (Xylanase
                                                                                            Score 663; DB 1; Pred. No. 7.7e-50;
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van Someren M.A., Voragen
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RESULT 11
Q12579 9PEZI
Q12579;
AC Q12579;
DT 01-NOV-1996 (TrEMBLrel.
DT 01-NOV-1996 (TrEMBLrel.
DT 01-MAR-2004 (TREMBLRE.
DC EUKARYOTER FUNG!; Ascommon Sordariomycetidae; Sord
OX NCBI TAXID=47794;
RN (1)
RN NUCLEOTIDE SEQUENCE.
RN MEDLINE=96118924; PubMer
RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two family G xylanase RT "Two fa
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PIR; S71472; S71472.

HSSP; P36217; 1XYO.

GO; GO:0031176; F:endo-1,4-beta-xylanase activity;
GO; GO:0005975; P:carbohydrate metabolism; IEA.

GO; GO:0045493; P:xylan catabolism; IEA.

GO; GO:0045793; P:xylan catabolism; IEA.

InterPro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PRINTS; PR00911; GLHYDRLASE11.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.

Glycosidase; Hydrolase; Xylan degradation.

SEQUENCE 219 AA; 23325 MW; 4729299E08FD9FBA CRO
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Eukaryota; Fungi; Ascomycota; Posordariomycetidae; Sordariales; NCBI_TaxID=47794;
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MEDLINE=96118924; PubMed=8595661; DOI=10.1007/BF00313196.
Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N
"Two family G xylanase genes from Chaetomium gracile and expression in Aspergillus nidulans.";
Curr. Genet. 29:73-80(1995).
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                                                                                                                      VNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGD
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Pred. No. 3.6e-49;
3; Mismatches 42
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                                                                                                                          HYYQIVATEGYFS 182
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                                                                                                                                                                                                                              CDGSIYRLGKTTR 122
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RESULT 12 013447_COCSA

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EMBL; AJ004802; CAA06151.1; -; Genomic_DNA
HSSP; Q8J1V6; 1H1A.

GO; GO:0004553; F:hydrolase activity, hydro
GO; GO:0005975; P:carbohydrate metabolism;
GO; GO:0045493; P:xylan catabolism; IEA.
InterPro; IPR001137; Glyco_hydro_11.
Pfam; PF00457; Glyco_hydro_11; 1.
PRINTS; PR00911; GLHYDRLASE11.
PROSITE; PS007776; GLYCOSYL_HYDROL_F11_1; 1.
Xylan degradation.
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Q70T28 9PLEO PRELIMINARY;
Q70T28;
Q70T28;
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
Xylanase precursor.
Name=xyl2;
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Mycol. Res. 105:352
EMBL; AJ004802; CAA
HSSP; Q8J1V6; 1H1A.
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O13447;
O1-JAN-1998 (TrEMBL
O1-JAN-1998 (TrEMBL
O1-OCT-2003 (TrEMBL
Beta-1,4-xylanase.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Pleosporales; Pleosporaceae; Cochliobolus.
NCBI_TaxID=45130;
NUCLEOTIDE SEQUENCE.

PubMed=15016446; DOI=10.1016/j.biochi.2004.01.001;

Degefu Y., Lohtander K., Paulin L.G.;

"Expression patterns and phylogenetic analysis of (htxyl 1 and htxyl 2) from Helminthosporium turcicules blight of maize.";

Biochimie 86:83-90(2004).

EMBL; AJ548879; CAD70174.1; -; Genomic_DNA.
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Cochliobolus
                                                                                                                                                                                                                                          Setosphaeria turcica.
Eukaryota; Fungi; Ascomycota;
Pleosporales; Pleosporaceae; Senti TaxID=93612;
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PRESULT 14

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O7SDQ1 NEUCR

O7SDQ1 NEUCR

O7SDQ1 NEUCR PRELIMINARY;

D7SDQ1 NEUCR

D7SDQ1 NEUCR

O7SDQ1 NEUCR

D7SDQ1 NEUCR

D7SDQ1 NEUCR

D7SDQ1 NEUCR

D7 O1-MAR-2004 (TrEMBLrel. 26, Last sequence updated of the protein (Probable endo-1, 4-beta-x gn Name=NCUU2855.1; Synonyms=B10D6.120;

Neurospora crassa.

OC Sukaryota; Fung1; Ascomycota; Pezizomycotina; Scordariomycetidae; Sordariales; Sordariaceae; N NCB1 TaxID=5141;

RN NCLEOTIDE SEQUENCE.

RN NUCLEOTIDE SEQUENCE.

RA NUCLEOTIDE SEQUENCE.

RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Pu RA Glaigan J.B., Calvo S.E., Borkovich K.A., Selke Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Pu RA Glaigan J.B., Calvo S.E., Borkovich K.A., Selke Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Pu RA Glaigan J.B., Calvo S.E., Borkovich K.A., Selke Selitrennikoff C.P., Kinsey J.A., Braun E.L., 2 Selitrennikoff C.P., Maxoc Roy A., Foley K., Naylor J., Thomann N., Barret RA Cogoni C., Macino G., Catcheside D., Li W., Pra DeSouza C.C., Glass L., Orbach M.J., Berglund J. RA Cogoni C., Macino G., Catcheside D., Li W., Pra DeSouza C.C., Glass L., Orbach M.J., Berglund J. RA Nature D.O., Alex L.A., Mannhaupt G., Ebbole D. RA Nature D.O., Sachs M.S., Lander E.S., Nusbaum C. "The Genome Sequence of the Filamentous Fungus RL Schulte U., Aign V., Hoheisel J., Brandt P., Fa Schulte U., Aign V., Hoheisel J., Brandt P., Fa Schulte U., Aign V., Hoheisel J., Brandt P., Fa Schulte U., Aign V., Hoheisel J., Brandt P., Fa Schulte U., Aign V., Hoheisel J., Brandt P., Fa Schulte U., Aign V., Hoheisel J., Brandt P., Fa Schulte U., Aign V., Hoheisel J., Brand
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Matches 115
                                                                                                                                                      PUCLEOTIDE SEQUENCE.

STRAIN=OR74A;

Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N. Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N. Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endri Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schu Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenb Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Fri Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Fri Kamal M., Kashuyssen C., Metzenberg R.L., Perkins D.D., K. Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osman DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aram Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M. Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.; "The Genome Sequence of the Filamentous Fungus Neurospora cra
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GO; GO:0004553; F:hydrolase activity, hydroly
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0045493; P:xylan catabolism; IEA.
InterPro; IPR001137; Glyco_hydro_11.
Pfam; PF00457; Glyco_hydro_11; 1.
PRINTS; PR00911; GLHYDRLASE11.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
Signal; Xylan degradation.
Signal; Xylan degradation.
SIGNAL 1 19 Potential.
SIGNAL 20 231 AA; 25611 MW; 44078D5BB52BAF
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Pred. No. 5.7e-49;
3; Mismatches 45
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C., Kroken S.,
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REMBL; BX842624; CAE76228.1; -; Genomic_DNA.

REMBL; BX842624; CAE76228.1; -; Genomic_DNA.

RESP; Q8J1V6; 1H1A.

REGO; GO:0004553; F:hydrolase activity, hydrolyzing O-g
REGO; GO:0005975; P:carbohydrate metabolism; IEA.

REGO; GO:0045493; P:xylan catabolism; IEA.

REGO; GO:0045493; P:xylan catabolism; IEA.

REGO; GO:00457; Glyco_hydro_11.

REFORM; PF00457; Glyco_hydro_11.

REFORM; PF00457; GLYCOSYL_HYDROL_F11_1; 1.

REPROSITE; PS007776; GLYCOSYL_HYDROL_F11_2; 1.

REPROSITE; PS007777; GLYCOSYL_HYDROL_F11_2; 1.

REPROSITE; PS007770; GLYCOSYL_HYDROL_F11_2; 1.
A Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
A Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
A Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
A Arroya J., Berriman M., Coulsen R., Davies R., Dyer P.S.,
A Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
A Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
A Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
A Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
A Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
A Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
A Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.
A Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
A Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
A Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
A Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
A Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares S.
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Matches 118
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13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence upda 13-SEP-2005 (TrEMBLrel. 31, Last annotation up Endo-1,4-beta-xylanase (XlnA), putative.
ORFNames=Afu3g00320;
Aspergillus fumigatus Af293.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiales; Trichocomaceae; mitosporic Trichocomceillus (Traxides);
(CBI Taxides); Ascomaceae; mitosporic Trichocomceillus (Traxides);
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German Neurospora genome project;

Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases
-i- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
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Pred. No. 9.8e-49;
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itosporic Trichocomaceae; Asperg
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, Bermejo c...
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Y., Fischer J
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rmejo C., Bennett J.,
ies R., Dyer P.S.,
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RT "Genomic sequence of the pathogenic and allergenic filamen Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
C -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which preliminary data.
EMBL; AAHF0100010; EAL86316.1; -; Genomic DNA SEQUENCE 228 AA; 24494 Note of the preliminary databases.
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                                       SGSASITV
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larity 61.7%;
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          10,
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, Asai K.,
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

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US-09-570-856B-29
US-08-044-621D-29
US-09-570-856B-18
US-09-570-856B-18
US-09-047-370-9
US-09-048-733-7
US-08-768-373-2
US-09-849-242A-2
US-09-047-370-14
US-08-709-912-16
US-08-709-912-16
US-08-121-436A-2
US-08-044-621D-26
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US-08-121-436A-2
US-09-570-856B-19
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| | Query M Best Lo Matches | INFOI SE(SE(MO) | TELLIN | C C C | CONTR | SULT 1 3-08-886-7 Sequence Patent No GENERAL APPLIO APPLIO APPLIO | | 4 4 4 4 1 4 4 4 0 10 4 0 | 2 2 2 2 3 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 2 2 2 2 2 2 2 8 8 9 9 9 9 9 9 9 9 9 9 9 |
| 1 32 | Match Local es 19 | TELEFAX: INFORMATION F SEQUENCE CH LENGTH: TYPE: am TOPOLOGY: MOLECULE TY 08-886-765-2 | CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Lambirie, Elias J REGISTRATION NUMBER: 33,7 REPERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATIC TELECOMMUNICATION INFORMATIC | COUNTRY: USA ZIP: 10174 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ FOR WI CURRENT APPLICATION DATA: APPLICATION NUMBER: US/O BILLING DATE: 1507 | APPLICANT: Kn. TITLE OF INVEN' NUMBER OF SEQUI CORRESPONDENCE ADDRESSEE: 1 STREET: 405 CITY: New Y. STATE: NY | 7 . 8.19.0 | | 562. 562. 552. | 574 572 571 571 | 630. 62 61 586. 574. 574. |
| 0-0 | Simi | PAX: 21 CON FOR E CHARA H: 225 amino OGY: 1 JE TYPE: | FICE/AGE | 10174 10174 R READ M TYPE TER: TING S: ARE: APPLIC | VIT: K F INVE F SEQ DUBBNC SSEE: G: 40 New New | ~ ~ _ | | ம் | ຜ ິທ ທ ທ ທ | |
| QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI | llarit Conse | FOR SEQ ID NO: CHARACTERISTICS 225 amino acid amino acid Y: linear TYPE: protein | ATION NOTE NOTE NOTE NOTE NOTE NOTE NOTE NO | USA 74 DABI 1BM SYST Fag 1CAT NU | | 65-2 2, Application 2, S817500 INFORMATION: ANT: Hansen, ANT: Wagner, ANT: Mullert: | | | | 58.0 56.7 53.9 52.9 52.8 |
| GWHD | ιγ γ | 12-878-99 SEQ ID SEQ ID ACTERIST Samino o acid linear prote | I: 4 NFOR NFOR UMBE UMBE IN IN | ABLE FOI I Diske I BM Comp YSTEM: YSTEM: PastSEQ CATION I NUMBER: | P, Inge ION: A NCES: ADDRESS lo. 5817 Lexingt | K K B P. | | | | |
| GYYY GYYY | 100. 100. tive | 212-878-9655 R SEQ ID NO: RACTERISTICS: 25 amino acids no acid linear E: protein | 4: 435 (INFORMATION: (INFORMATION: (IS, Elias J (IUMBER: 33,728 (ET NUMBER: 43)N INFORMATION: | Diskette Diskette Compatil Compatil Compatil Compatil Compatil USBA DOS DATA DOS DATA | p, Inge Helmer PION: Animal Fee ENCES: 2 ADDRESS: 0 No. 58175000 No. Lexington Avenue ork | יסיטי • | | 189 206 191 191 344 | 296 231 215 215 335 | 2225 2225 2225 2225 2225 2225 2225 222 |
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US-09-115-660-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/115
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,76.
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
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SOFTWARE: PastSEQ for Windows Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62455460 No. 6245546disk of No.
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                                                                                   HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
                                                                                                                                             QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI
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                                                                HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT
                                                                                                                              QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI
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Mullertz, Anette
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100.0%; Pred. No. 4e-97;
tive 0; Mismatches 0;
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US-09-570-856B-23
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Patent No. 6bozz-
Patent INFORMATION:
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SOFTWARE: PatentIn versionsEQ ID NO 24
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                                                             SOFTWARE: POSEQ ID NO 23
                                                                                                       APPLICANT: Bentzien, Joerg M
APPLICANT: Dahiyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANA
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 199-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dahiyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANAS
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
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                                                                          NUMBER OF SEQ ID NOS: SOFTWARE: Patentin ve
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NAME/KEY: MISC FEATURE
LOCATION: (1)...(1)
OTHER INFORMATION: "Xaa
                               LENGTH: 194
TYPE: PRT
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              ORGANISM: Paecilomyces variotii
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Bassil I
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RESULT 6
US-08-044-621D-29
; Sequence 29, Application Us
; Patent No. 5405769
; GENERAL INFORMATION:
; APPLICANT: Warren W. W;
APPLICANT: Wing L. Sun;
APPLICANT: Robert L. C
; APPLICANT: David R. Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-09-570-8568-29
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; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Cochliobolus c
US-09-570-8568-29
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Best Local 8
Matches 133
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APPLICANT: Bentzien, Joerg M
APPLICANT: Dahiyat, Bassil I

TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
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Best Local S
Matches 169
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al Similarity 87.6%;
169; Conservative 1
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                                                                                                                                                                                                                                                                                                                    TYSGTYNYNGNSYLAVYGWTRNPLVEYYVVENFGTYDPSSQSQNKGTVTSDGSSYKIAQS
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   Warren W. Wakarchuk
Wing L. Sung
Makoto Yaguchi
Robert L. Campbell
David R. Rose
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                                                                 Wakarchuk
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Pred. No. 9.6e-64;
2; Mismatches 33
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Pred. No. 2.4e-85;
L; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
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; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
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US-08-044-621D-29
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MOLECULE TYPE:

MOLECULE TYPE:

DESCRIPTION: prote
HYPOTHETICAL: No
"NTI-SENSE: No
"VPE: No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erratt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/
FILING DATE: April 8, 1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowling, St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE:
ORGANISM: Schi
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Schizophyllum STRAIN: Schizophyllum cc
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION:
AUTHORS: Oku T., Yaguchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                             POSITION IN GENOME:
                                                                                                                                                                                                                                                                                VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                               AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
STRANDEDNESS: No.
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                                    62
                                                                                                                                             Similarity
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K1P 1C3
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    TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGI
                                                                 TPSSTGTDGGYYYSWWTDGAGDATYQNNGGGSYTLTWSGNNGNLVGGI
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Suite 2600,
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                                                                                                                            60.9%; Score 663; DB 1; 61.3%; Pred. No. 3.4e-56; tive 26; Mismatches 43
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160 Elgin Street
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
TENGTH: 197 amino acids
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                                           Query Match
Best Local (
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                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION INFORMATION
TELEPHONE: (212) 758-2400
TELEPAX: (212) 758-2982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermoshilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                            FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                    STRAIN: Xylanase A PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
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                                                                                                              JOURNAL:
                                                                                                                                                                        AUTHORS:
                            Local Similarity
mee 119; Conserv
                                                                                                    DATE:
                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                              AUTHORS:
                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                             AUTHORS
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                                                                                                              S: Parse, M
S: Jurasek, L
L: Canadian Fed.
Abstract #676
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                                                                                                    1988
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  TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGWNPGLNARAIH 61
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PE: internal
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                              Conservative
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NO
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758-2982
30. 9:
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                                          Score 663;
Pred. No. 3.
                                                                                                                                Soc.
                              Mismatches
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                                          DB 1;
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                           43;
                                                       Length 197;
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                              6;
                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                            TELEFAX: (212) 758-29
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yaguchi D
APPLICANT: Ishikawa
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                     ORGANISM: Sc...
STRAIN: Xylanase A
STRAIN: INFORMATION:
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                                                                        PUBLICATION
                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                ANTI-SENSE:
AUTHORS:
AUTHORS:
JOURNAL:
                                                                                                                                                                                   TYPE: STRANDEDNESS: SIT
                                                                                                                                                                                                                                                                                                                                     NAME: Olsen Mr, Warren REGISTRATION NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                        AUTHORS:
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                                                                                                                                 TYPE:
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                             Yaguchi,
Parse, M
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Yaguchi Dr., Makoto
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                                                                                                    Schizophyllum
 Jurasek, L
Canadian Fed.
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Modification of Xylanase to Improve
Thermophilicity, Alkalophilicity and
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KGWNPGAASRSIS
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APPLICANT: Bentzien, Joerg M
APPLICANT: Dahiyat, Bassil I
ITITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYL
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 197
        RESULT 10
US-08-458-023B-4
/ Sequence 4, Application US/08458023B
/ Patent No. 5667990
/ GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                / TYPE: PRT; ORGANISM: Schizophyllum US-09-570-856B-18
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US-09-570-856B-18
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US-09-047-370-9
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GENERAL INFORMATION:
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Best Local Similarity
Matches 119; Conserva
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Best Local Similarity
Matches 119; Conserv
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                                                                                                        TEGYOSSGTATITY
                                                                                                                                  TEGYFSSGYARITY 190
                                                                                                                                                             RYNAPSIDGTQTFEQFWSVRNPKKAPGGSISGTVDVQCHFDAWKGLGMNLGSEHNYQIVA
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Randy
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61.3%; Pred. No. 3.4e-56;
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Pred. No. 3.4e-56;
6; Mismatches 43
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                                                                                                                                                                                                                                                                                                                                                  Length 197;
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GENERAL INFORMATION:
APPLICANT: WATANABE, MANABU
APPLICANT: MORIYA, TATSUKI
APPLICANT: MORIYA, TATSUKI
APPLICANT: MOYAGI, KAORU
APPLICANT: SUMIDA, NAOMI
APPLICANT: MURAKAMI, TAKESHI
TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE cbt
TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR
TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
FILE REFERENCE: 99-0266*/LC(WMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07
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US-09-254-733-7
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TELEPHONE: 212-80,
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                      Sequence 7, Application US/09254733 Patent No. 6277596
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ZIP: 10174-6201
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
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NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086.010-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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TITLE OF INVENTION: ASPERGILLUS EXPRESSION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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CITY: New York
STATE: New York
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US-08-768-373-2
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TITLE OF INVENTION: AND USES THENEL.

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FO. ADDRESSEE: STERNE, GOLDSTEIN & FO. ADDRESSEE: GOLDSTEIN & 
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SEQ ID NO 7
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Best Local Similarity 60.2
Matches 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn Ver. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:
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TYPE: PRT
ORGANISM: TRICHODERMA VIRIDE MC300-1
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5, 6228629
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T: LAHTINEN, TARJA
IT: LAHTINEN, TARJA
NT: FAGERSTR M, RICHARD
NT: SUOMINEN, PIRKKO
DF INVENTION: NOVEL XYLANASES, GF
TYPENTION: AND USES THEREOF
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VEHMAANPER , JARI
LANTTO, RAIJA
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Pred. No. 9.4e-54;
7; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version
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US-09-849-242A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09849242A Patent No. 6635464 GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: pir-
MOLECTI
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
APPLICATION NUMBER: US/09/849,242A
FILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION OBTA:
APPLICATION STANDARD: 508/768,373
APPLICATION NUMBER: US 08/768,373
FILING DATE: 17-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein LOCATION: 1..261 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN:
                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GO
STREET: 1100 NEW YORK AVENUE,
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PALOHEIMO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150
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STATE: L.
COUNTRY: US
COUNTRY: US
20005-3934
TO: 20005-3934
FJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSSATGTHNGYYYSFWTDGQGNIRFNLESGGQYSVTWSGNGNWVGGKGWNPGTDNRVINY 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Chaetomium CBS730.95
                                                                                                                                                                                                                                                                                     HT: PALOMETRO, ...
HAKOLA, SATU
MONTYLO, ARJA
VEHMAANPERO, JARI
LANTTO, RAIJA
LAHTINEN, TARJA
LAHTINEN, TARJA
FAGERSTRIM, RICHARD
SUOMINEN, PIRKKO
SUOMINEN, PIRKKO
AND USES THEREOF
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Pred. No. 1.4
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                                                                                                                                                                                                                                     GOLDSTEIN 60
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                                                                                                                                                                                                                                                                                                           GENES
                                                                                                        Version
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LOCATION: 1.261

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OTHER INFORMATION: /]
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SEQUENCE DESCRIPTION: SEQ
US-09-849-242A-2
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US-08-044-621D-28
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Best Local Similarity 60.1%;
Matches 113; Conservative 2
                                                                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/08044621D Patent No. 5405769
                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Warren W. Wakarchuk

APPLICANT: Wing L. Sung

APPLICANT: Makoto Yaguchi

APPLICANT: Makoto Yaguchi

APPLICANT: Robert L. Campbell

APPLICANT: David R. Rose

TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS

TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Gowling, Strathy & Henderson

GTBEST: Suits Season
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1716.0540004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
                                                                                                  STREET: Suite 2
CITY: Ottawa
STATE: Ontario
COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/008,746
PILING DATE: 18-DEC-1995
APPLICATION NUMBER: US 60/020,839
PILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGSATVNV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                  E: Gowling, Strathy & Henderson
Suite 2600, 160 Elgin Street
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 PC-DOS
                                  5.25
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; Pred. No. 1.4e-53;
27; Mismatches 47;
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3Q ID NO: 2:
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                                  360kB storage
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RESULT 15
US-08-709-912-14
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; PUBLICATION DATE:
; RELEVANT RESIDUES
US-08-044-621D-28
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.7
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Judy A. Erratt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
ANTI-SENSE: NO
ANTI-TYPE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/G
FILING DATE: April 8, 19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma harzianum
STRAIN: Trichoderma harzianum, 2
IMMEDIATE SOURCE:
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DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                              PAGES: 435-
DATE: 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                          ISSUE:
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                                                                                                                                                                                                                                                                                                                                                                                     DOCUMENT NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                              TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
                                                                                                                                                                                                                                  QTTPNSEGWHDGYYYSWWSDGGAQATYTNLÈGGTYEISWGDGGNLVGGKGWNPGLNARAI 60
                                                                                                          QRVNQPSIIGTATFYQYWSVRRNHRSSGSVNTANHFNAWASHGLTL-GTMDYQIVAVEGY 179
                                                                                                                                                                                                                   QTIGPGTGYSNGYYYSYWNDGHAGVTYTNGGGGSFTVNWSNSGNFVGGKGWQPGTKNKVI 60
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                                                       FSSGSASITVS
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Senior D.J., & S
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                                                                                                                                                                                                                                                                        Score 636.5; DB 1
Pred. No. 1.2e-53;
7; Mismatches 47
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Sequence 14,

Application US/08709912

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ZIP: 10172-0194

ZIP: 10172-0194

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr. Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEPAX: (212) 758-2400
TELEPAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acide
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Thrichoderma harzi
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Rollin, F
AUTHORS: Rollin, F
AUTHORS: Tan, L. U. L.
AUTHORS: Senior, D. J.
AUTHORS: Saddler, J. N.
JOURNAL: Xylan and Xylanase
PAGES: 435-438
DATE: 1992
3-709-912-14
                                                                                                                                                                                                                                  Query Match 58.5%; Score 636.5; DB 1; Best Local Similarity 60.7%; Pred. No. 1.2e-53; Matches 116; Conservative 27; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Sung D
APPLICANT: Yaguch
APPLICANT: Ishika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatric, Cella, Harper, and Scinto
STREET: 277 Park Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 277 Park
CITY: New York
STATE: New York
COUNTRY: USA
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TOPOLOGY: lir
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                                                                            QRVNQPSIIGTATFYQYWSVRRNHRSSGSVNTANHFNAWASHGLTL-GTMDYQIVAVEGY 179
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linear
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Qy 181 FSSGYARITVA 191
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Db 180 FSSGSASITVS 190
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Search completed: February 10, 2006, 15:03:37 Job time: 33.8735 secs

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length: 2000000000
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Match
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 Published Applications AA_Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

1: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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US-10-307-441-20
US-11-088-725A-46
US-09-467-368-2
US-10-237-386-24
US-10-237-386-21
US-10-425-115-221836
US-10-425-115-267585
US-10-425-115-361946
US-10-307-441-9
US-10-307-441-9
US-10-237-386-23
US-10-237-386-23
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US-10-307-441-19
US-10-237-386-32
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20, Appl
46, Appl
21, Appl
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21, Appl
221836,
227, Appl
361946,
9, Appl
36, Appl
23, Appl
26, Appl
27, Appl
26, Appl
27, Appl
28, Appl
21, Appl
26, Appl
27, Appl
28, Appl
31, Appl
32, Appl
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 |
|------------------|-------------------|-------------------|-------------------|------------------|------------------|------------------|-----------------|-----------------|------------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|-------------------|
| 562.5 | 562.5 | 562.5 | 568 | 568 | 571 | 573 | 576 | 576 | 585.5 | 604 | 609 | 616 | 623.5 | 624.5 | 630 | 630.5 | 632.5 |
| 51.7 | 51.7 | 51.7 | 52.2 | 52.2 | 52.5 | 52.7 | 52.9 | 52.9 | 53.8 | 55.5 | 56.0 | 56.6 | 57.3 | 57.4 | 57.9 | 58.0 | 58.1 |
| 228 | 191 | 191 | 189 | 189 | 240 | 313 | 223 | 223 | 223 | 221 | 233 | 225 | 223 | 190 | 221 | 190 | 190 |
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| US-10-237-386-39 | US-11-088-725A-38 | US-10-307-441-10 | US-11-088-725A-40 | US-10-307-441-13 | US-10-237-386-42 | US-10-213-990-72 | US-11-154-793-2 | US-10-299-393-2 | US-10-237-386-34 | US-10-237-386-44 | US-10-237-386-28 | US-10-237-386-36 | US-10-237-386-30 | US-11-088-725A-1 | US-10-213-990-66 | US-10-237-386-33 | US-11-088-725A-42 |
| Sequence 39, | Sequence 38, 1 | Sequence 10, Appl | Sequence 40, A | Sequence 13, A | Sequence 42, A | Sequence 72, A | Sequence 2, Ap | Sequence 2, Ap | Sequence 34, A | Sequence 44, A | Sequence 28, A | Sequence 36, A | Sequence 30, App | Sequence 1, Appli | | • | Sequence 42, App |

ALIGNMENTS

RESULT 1 US-10-307-441-20

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APPLICANT: SUNG, Wing L.

APPLICANT: National Research Council of Canada

TITLE OF INVENTION: Modified Xylanases Exhibiting Inc

TITLE OF INVENTION: and Alkalophilicity

FILE REFERENCE: 027367-5006US

CURRENT APPLICATION NUMBER: US/10/307,441

CURRENT FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: PCT/CA01/00769

PRIOR FILING DATE: 2001-05-31

PRIOR APPLICATION NUMBER: 60/213,803

PRIOR APPLICATION NUMBER: 60/213,803

PRIOR FILING DATE: 2000-05-31

NUMBER OF SEQ ID NOS: 51

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 20
RESULT 2
US-11-088-725A-46
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; TYPE: PRT
; ORGANISM: Thermomyces lanuginosus
US-10-307-441-20
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Best Local
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                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 194; Conservat
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TRVNAPSI
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                                                                   FSSGYARITVADVG
                                                                                                                                                                   TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNC
                                                                                                                                                                                                                         HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTV
                                                                                         FSSGYARITVADVG 194
                                                                                                                                                                                                       HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGT
                                                                                                                                                                                                                                                                     QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISI
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                                                                                                                                                                                                                                                                                                                                    100.0%; llarity 100.0%; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                    Length
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Sequence 46, Application US/11088725A Publication No. US20050214410A1 GENERAL INFORMATION:

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APPLICANT: logen Blo-rrung APPLICANT: White, Theresa C APPLICANT: White, Theresa C APPLICANT: Giroux, Genevieve R APPLICANT: Giroux, Genevieve R APPLICANT: Wallace, Katie E.A.

TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression FILE REFERENCE: Q80712

CURRENT APPLICATION NUMBER: US/11/088,725A

CURRENT FILING DATE: 2005-03-25

PRIOR APPLICATION NUMBER: US 60/556,061

PRIOR APPLICANT: Wallace Exhibiting Improved Expression FILE NUMBER: US 60/556,061

PRIOR APPLICANT: Wallace Exhibiting Improved Expression FILE NUMBER: US 60/556,061

PRIOR APPLICANT: Wallace Exhibiting Improved Expression FILE NUMBER: US 60/556,061

PRIOR APPLICATION: Wallace Exhibiting Improved Expression FILE NUMBER: US 60/556,061

PRIOR APPLICATION: Wallace Exhibiting Improved Expression FILE NUMBER: US 60/556,061

PRIOR APPLICATION: Wallace Exhibiting Improved Expression FILE NUMBER: US 60/556,061

PRIOR APPLICATION: Wallace Exhibiting Improved Expression FILE NUMBER: US 60/556,061

PRIOR APPLICATION UNMBER: US 60/556,
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US-09-467-368-2
US-09-467-368-2
; Sequence 2, Application US/09467368
; Patent No. US20020160080A1
; GENERAL INFORMATION:
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        COUNTRY: USA
ZIP: 10174

ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.(
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,368
FILING DATE: 21-Dec-199
CLASSIFICATION EVINNOWN>
PRIOR APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
THE STRATION NUMBER: 33,728
THE STRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hansen, Peter Kamp
Wagner, Peter
Mullertz, Anette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS: No. US20020160080A1o No. US20020160080A1disk of No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 405 Lexington Avenue CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSSGYARITVADVG 194
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NUMBER:
4324.204-US
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GENERAL INFORMATION:

APPLICANT: Danisco A/S

APPLICANT: Sibbesen, Ole

APPLICANT: Sorensen, Jens

TITLE OF INVENTION: Xylanse Variants Having

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/10/237,386

CURRENT FILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR PILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-06-27

PRIOR FILING DATE: 2000-06-27
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US-10-237-386-24
; Sequence 24, Application US/10237386
; Publication No. US20030180895A1
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; ORGANISM: T.
US-10-237-386-24
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Best Local Similarity
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Best Local :
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SOFTWARE: PatentIn versi
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TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ
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121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
                                        92
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                                                                                                     FSSGYARITVADVG 194
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Conservative 0;
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Pred. No. 2e-97;
; Mismatches 0;
                                                                                                                                                               Score 1088; DB 4;
Pred. No. 2e-97;
Mismatches 0;
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/ECDGSIYRLGKT 151
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Sequence 20, Application US/10237386;
Publication No. US20030180895A1

GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Jens
TITLE OF INVENTION: Xylanse Variants Having Alt
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 000585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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US-10-237-386-20
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US-10-237-386-21
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/ ORGANISM: H.
US-10-237-386-21
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TITLE OF INVENTION: Xylanse Variants Having
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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SEQ ID NO 21
LENGTH: 227
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Best Local Similarity
Matches 136; Conserva
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
FITTLE OF INVENTION: Nucleic Acid
FILE REFERENCE: 38-21(53222)B
FILE REPPLICATION NUMBER: US/10/
CURRENT APPLICATION NUMBER: US/10/
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 221836
LENGTH: 227
TYPE: PRT
ORGANTON
                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION:
US-10-425-115-221836
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US-10-425-115-221836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT; ORGANISM: C. US-10-237-386-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 221836, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yongwei
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                                                                                TYSGSYNPNGNSYLAIYGWTRNPLVEYYVVENFGTYDPSSQASNKGT
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                                                               TRINGPSIDGIRTFQQYWSVRQNKRSSGSVNMKTHFDAWASKGMTL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYSGTYNYNGNSYLAVYGWTRNPLVEYYVVENFGTYDPSSQSQNKGT
 FSTGSASITV
                                FSSGYARITV 190
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224
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70.0%; Pr
tive 22;
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                                                                                                                                                                                                                                                                Score 737; DB 4;
Pred. No. 2.7e-63;
8; Mismatches 32
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Pred. No. 8.5e-64;
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VTADGSSYKIAQS 155
                                                                                                                                                                                                GKGWNPG-SARTV 95
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                                                                  SHYYQIVATEGY 214
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APPLICANT: Sibbeen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sen
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
LENGTH: 227
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 267585
LENGTH: 221
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US-10-237-386-22
; Sequence 22, Application US/102:
; Publication No. US20030180895A1
; GENERAL INFORMATION:
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; ORGANISM: A. US-10-237-386-22
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Best Local
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NAME/KEY: unsure
LOCATION: (1)..(221)
OTHER INFORMATION: un
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
                                     LENGTH:
TYPE: PR
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al Similarity 68.4%;
130; Conservative 2:
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FSTGNGQITV
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules a
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 361946
LENGTH: 234
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US-10-425-115-361946
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US-10-307-441-9
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; OTHER INFORMATION:
US-10-425-115-361946
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Best Local S
Matches 130
Sequence 9, Application US/10307441
Publication No. US20030166236A1
GENERAL INFORMATION:
APPLICANT: SUNG, Wing L.
APPLICANT: National Research Countrille Of INVENTION: Modified Xylan
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                            EGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTR 122
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                                                                                                                                   SGSSSITV
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  Yylanases Exhibiting
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Pred. No. 9.7e
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    MRT4577_93271C.1.pep
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Pred. No. 7.5e-61;
4; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecules
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9.7e-62;
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ADGSSYKIAQTQR 161
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   d Thermophilicity
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CURRENT APPLICATION NUMBER: US/10/307,441
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: PCT/CA01/00769
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/213,803
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 51
SOPTWARE: Patentin Ver. 2.1
SQPTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                     ; LENGTH: 197
; TYPE: PRT
; ORGANISM: Schizophyllum commune
US-11-088-725A-36
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US-11-088-725A-36
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; ORGANISM: Schizophyllum commune
US-10-307-441-9
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Best Local Similarity
Matches 119; Conser
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Best Local Similarity 61.3
Matches 119; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: logen Bio-Products Corporation
APPLICANT: white, Theresa C
APPLICANT: white, Theresa C
APPLICANT: Giroux, Genevieve R
APPLICANT: wallace, Katie E.A.
TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression
FILE REFERENCE: Q80712
CURRENT APPLICATION NUMBER: US/11/088,725A
CURRENT FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 60/556,061
PRIOR PILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 46
NUMBER OF SEQ ID NOS: 46
NUMBER OF SEQ ID NOS: 46
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122 RVNAPSIDGTQTFDQYWSVRQDKRT----SGTVQTGCHFDAWARAGLNVNGDHYYQIVA 176
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                                                                                                                                     TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGWNPGLNARAIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEGYQSSGTATITV 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYNAPSIDGTQTFEQFWSVRNPKKAPGGSISGTVDVQCHFDAWKGLGMNLGSEHNYQIVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVNAPSIDGTQTFDQYWSVRQDKRT-----SGTVQTGCHFDAWARAGLNVNGDHYYQIVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGWNPGLNARAIH
                                       YSGTYQPNGNSYLSVYGWTRSSLIEYYIVESYGSYDPSSAASHKGSVTCNGATYDILSTW 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/11088725A
                                                                                                                                                                                          60.9%; llarity 61.3%; Conservative 26
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                                                                                                                                                                                        ; Score 663; DB 6;
; Pred. No. 3.5e-56;
26; Mismatches 43
                                                                                                                                                                                          43;
                                                                                                                                                                                                                              Length 197;
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APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivit
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
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US-10-237-386-29
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; ORGANISM: S.
US-10-237-386-23
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APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having All
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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SEQ ID NO 23
LENGTH: 201
                                                                                                                                                                                                                                Sequence 29, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVE
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Sequence 26, Application US/10237386

Publication No. US20030180895A1

GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhil
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3
; SEQ ID NO 29
; LENGTH: 219
; TYPE: PRT
; ORGANISM: C. gracile
US-10-237-386-29
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; TYPE: PRT
; ORGANISM: C. (
US-10-237-386-26
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                                                                                                                                                                                                                                       Query Match 60.3%; Score 656; DB 4; Length 231; Best Local Similarity 61.1%; Pred. No. 2.1e-55; Matches 116; Conservative 27; Mismatches 45; Indels
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                                                                                                                                                                       OSTPSSEGYHNGYFYSWWTDGGGSAQYTMGEGSRYSVTWRNTGNFVGGKGWNPG-TGRVI
                                                                                                                                                                                        SGYARITVA 191
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FSSGYARITY 190
                                                       TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
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                                  TRYNQPSIDGTRTFQQYWSVRQQKRVGGSVNMQNHFNAWSRYGLNL-GQHYYQIVATEGY
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Search completed: February 10, 2006, 15:22:35 Job time: 113.437 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of hits satisfying chosen parameters:
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1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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 13122538 residues
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261.826 Million cell updates/sec
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| 512.5 | 520.5 | 521 | 522.5 | 524 | 526.5 | 531 | 532.5 | 533.5 | 535 | 537 | 541 | 543.5 | 544 | 554 | 554 | 555.5 | 560 | 560 | 560 |
| 47.1 | 47.8 | 47.9 | 48.0 | 48.2 | 48.4 | 48.8 | 48.9 | 49.0 | 49.2 | 49.4 | 49.7 | | | 50.9 | | 51.1 | 51.5 | 51.5 | 51.5 |
| 346 | 358 | 225 | 237 | 445 | 347 | 303 | 216 | 542 | 352 | 358 | 354 | 240 | 241 | 242 | 239 | 221 | 344 | 301 | 220 |
| 6 | σ | σ | 7 | Φ | σ | σ | 7 | σ | σ | თ | σ | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 |
| US-10-517-939-160 | US-10-517-939-370 | US-10-517-939-172 | US-11-170-653-47 | US-10-517-939-368 | US-10-517-939-196 | US-10-517-939-214 | US-11-170-653-45 | US-10-517-939-262 | US-10-517-939-226 | US-10-517-939-182 | US-10-517-939-216 | US-11-170-653-38 | US-11-170-653-43 | US-11-170-653-41 | US-11-170-653-40 | US-11-170-653-37 | US-11-108-163B-10 | US-11-108-163B-11 | US-11-108-163B-12 |
| Sequence 160 | Sequence 370 | Sequence 17 | Sequence 47, | Sequence 36 | Sequence 19 | Sequence 21 | Sequence 45, | Sequence 262 | Sequence 22 | Sequence 182 | Sequence 216 | Sequence 38 | Sequence 43 | Sequence 41 | Sequence 40 | Sequence 37 | Sequence 10 | Sequence 11 | Sequence 12 |
| • | • | | 7, Appl | | | | | | • | 32, App | • | • | • | • | • | • | • | ., Appl | Appl |

APPLICANT: Sibbesen, Ole APPLICANT: Sorensen, Jens TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivit FILE REFERENCE: 674509-2046 CURRENT APPLICATION NUMBER: US/11/170,653 CURRENT FILING DATE: 2005-06-23 PRIOR APPLICATION NUMBER: US/10/237,386 PRIOR FILING DATE: 2002-09-09 PRIOR APPLICATION NUMBER: PCT/IB01/00426 PRIOR FILING DATE: 2001-03-08 PRIOR FILING DATE: 2000-03-08 PRIOR PILING DATE: 2000-03-08 PRIOR APPLICATION NUMBER: GB 0005585.5 PRIOR PILING DATE: 2000-03-08 PRIOR PILING DATE: 2000-06-27 NUMBER OF SEQ ID NOS: 66 Sequence 24, Application US/11170653 Publication No. US20050271769A1 GENERAL INFORMATION: APPLICANT: Danisco A/S APPLICANT: Sibbesen, Ole APPLICANT: Sorensen, Jens SOFTWARE: P 3.0 ivity to Xylanase Inhibitors

RESULT 1 US-11-170-653-24

ALIGNMENTS

; LENGTH: 225 ; TYPE: PRT ; ORGANISM: T. ; ORGANISM: T. US-11-170-653-24

lanuginosus

PatentIn

version

Query Match Best Local Similarity Matches 194; Conserv

100.0%; ilarity 100.0%; Conservative 0;

Score 1088; DB 7; Pred. No. 1.7e-93; Mismatches 0;

Length

225;

0; Gaps

0;

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FSSGYARITVADVG 194

FSSGYARITVADVG

92 61 32

HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTV

HFEGVYOPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGT

TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNG

DHYYOIVATEGY 211

ECDGSIYRLGKT 151 DHYYQIVATEGY 180

ECDGSIYRLGKT 120

QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVG

QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVG

GKGWNPGLNARAI 60

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RESULT 2
US-11-170-653-21
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APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having All
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/11170653 Publication No. US20050271769A1 GENERAL INFORMATION:
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Best Local (
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APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitoz
FILE REFERENCE: 674509-2046
CURRENT FILING DATE: 2005-06-23
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: GB 0015751.1 PRIOR FILING DATE: 2000-06-27 NUMBER OF SEQ ID NOS: 66
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                                                                                                                                                                                                                                                                                                                                APPLICANT: Danisco A/S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRTNOPSIDGTRTFQQYWSVRQNKRSSGSVNMKTHFDAWASKGMNL-GSHYYQIVATEGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSSGYARITY 190
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10. US20050271769A1
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Pred. No. 4.7e-63;
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GENERAL INFORMATION:

APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Jens
TITLE OF INVENTION: Xylanse Variants Having All
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
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US-11-170-653-22
Sequence 22, Appl
Publication No. L
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Best Local Similarity
Matches 133; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 227
TYPE: PRT
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                                                                                                                                                                                                              TPSSQGTHNGCFYSWWTDGGAQATYTNGAGGSYSVNWKTGGNLVGGKGWNPGA-ARTITY 97
                                                                                                                                                                                                                                TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHF 62
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                                                                                         VNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFS 182
                                                                                                                                          SGYARITY 190
                                                                    TNOPSIDGTQTFQQYWSVRQNKRSSGSVNMKTHFDAWAAKGMKL-GTHNYQIVATEGYFS 216
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 SGSAQITV
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224
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Pred. No. 1.4e-61;
2; Mismatches 33
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GQHYYQIVATEGY 208
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TITLE OF INVENTION: Xylanse Variants Having FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Pacentin version 3.0
SEQ ID NO 23
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US-11-170-653-23
; Sequence 23, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
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US-11-170-653-29
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APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Alt
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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Best Local S
Matches 119
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TYPE: PRT
ORGANISM: S.
-11-170-653-23
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                                                                                                                                                                                                                                                                      APPLICANT: Danisco A/S
APPLICANT: Sibbesen, (
APPLICANT: Sorensen, (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variants Having Altered Sensitivity to Xylanase Inhibitor
                                                                                                                                                                                                                                                      Altered Sensitivity to Xylanase Inhibito
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; LENGTH: 219
; TYPE: PRT
; ORGANISM: C. (
US-11-170-653-29
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; TYPE: PRT
; ORGANISM: C. :
US-11-170-653-26
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US-11-170-653-26
; Sequence 26, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
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APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 26
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                                                                                                                                                                                                                                                                                  Query Match 60.3%; Score 656; DB 7; Best Local Similarity 61.1%; Pred. No. 1.2e-53; Matches 116; Conservative 27; Mismatches 45
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Best Local Similarity
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APPLICANT: Sibbesen, (
                                                                                                                                  100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117;
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                                                                            TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
                                                                                                                                                                                                                                          QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHF 62
                                                                                                                                                                                                          VNQPSIEGTSTFDQFWSVRQNHRSSGSVNVAAHFNAWAQAGLKL-GSHNYQIVATEGYQS 210
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                                                                                                                                                                                                                                                                                                                         Length 231;
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                                                           GHYYQIVATEGY 218
                                                                                                                                                                                                        SKGWNPG-TGRVI 99
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                                                                                                                                QTDGGTYNVAVS 159
                                                                                                                                                                     ECDGSIYRLGKT 120
                                                                                                                                                                                                                                                                                    2; Gaps
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; TYPE: PRT; ORGANISM: C. US-11-170-653-25
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US-11-170-653-27
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                      CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
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LENGTH: 231
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Best Local
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TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
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APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having
FILE REFERENCE: 674509-2046
  NUMBER
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APPLICANT: Sibbesen, (
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Sorensen, Jens
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Pred. No. 6.7e-53;
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; TYPE: PRT
; ORGANISM: H.
US-11-170-653-27
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Best Local (
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YFSSGYARITV 190
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; SOFTWARE: PatentIn version 3
; SEQ ID NO 35
; LENGTH: 241
; TYPE: PRT
; ORGANISM: C. gracile
US-11-170-653-35
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APPLICANT: Sorensen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivit
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
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Best Local Similarity 59.4
Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGG
                                                                                                                                                      OSSGESDIYV 224
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                                                                                                                                                                                                                                                                                                                             QTLTSSQTGTNNGYYYSFWTDGQQNQQYTNEAGGQYSVTWSGNGNWV
                                                   TTRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/11170653
No. US20050271769A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.1%; Score 642.5; DB 7; 61.8%; Pred. No. 2.2e-52; ive 27; Mismatches 43;
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Pred. No. 1e-52;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                GKGWNPG-SART 89
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GTHDYQIVATEG 208
                                                                                                                                                                                                                                                                                                                                                                      GKGWNPGLNARA 59
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                                                                GDHYYQIVATEG 179
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RESULT 12
US-11-170-653-31
; Sequence 31, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
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US-11-170-653-32
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APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Al:
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR PILING DATE: 2000-06-27
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Best Local S
Matches 115
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Publication No. US20050271769A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 32
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TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
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les 115; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93
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                                                                                                                                                                                                                       Altered Sensitivity to Xylanase Inhibitor
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; LENGTH: 223
; TYPE: PRT
; ORGANISM: T.
US-11-170-653-31
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ITITLE OF INVENTION: Xylanse Variants Having Altered Sensitivit
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.1
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
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US-11-170-653-33
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SEQ ID NO 33
LENGTH: 190
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                                                                                                                                                                                                                                                           Query Match 58.0%; Score 630.5; DB 7; Best Local Similarity 60.2%; Pred. No. 2.2e-51; Matches 115; Conservative 27; Mismatches 48;
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Best Local Similarity
Matches 115; Conser
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                                   121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
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                                                                                 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGY 180
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                                                                                                                                                                                              QTTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAI 60
                                                                                                                                                                         QTIGPGTGYSNGYYYSYWNDGHAGVTYTNGGGGSFTVNWSNSGNFVAC
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60.2%; Pred. No. 9.1e-52;
cive 28; Mismatches 47
                                                                                                                                                                                                                                                                                                  Length
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TMDÝQIVÁVEGÝ 179
                                                                                                                                                                        KGWQPGTKNKVI 60
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GENERAL INFORMATION:

APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to 3
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanse Variants Having Alt
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 223
TYPE: PRT
ORGANISM: T. reesei
US-11-170-653-30
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US-11-170-653-36
US-201-653-36
Sequence 36, Application US/11170653
Publication No. US20050271769A1
GENERAL INFORMATION:
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US-11-170-653-30
; Sequence 30, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
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APPLICANT: Sibbesen, (
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